

SUPPLEMENTAL DATA

**JAM3: A prognostic biomarker for bladder
cancer via epithelial–mesenchymal transition
regulation**

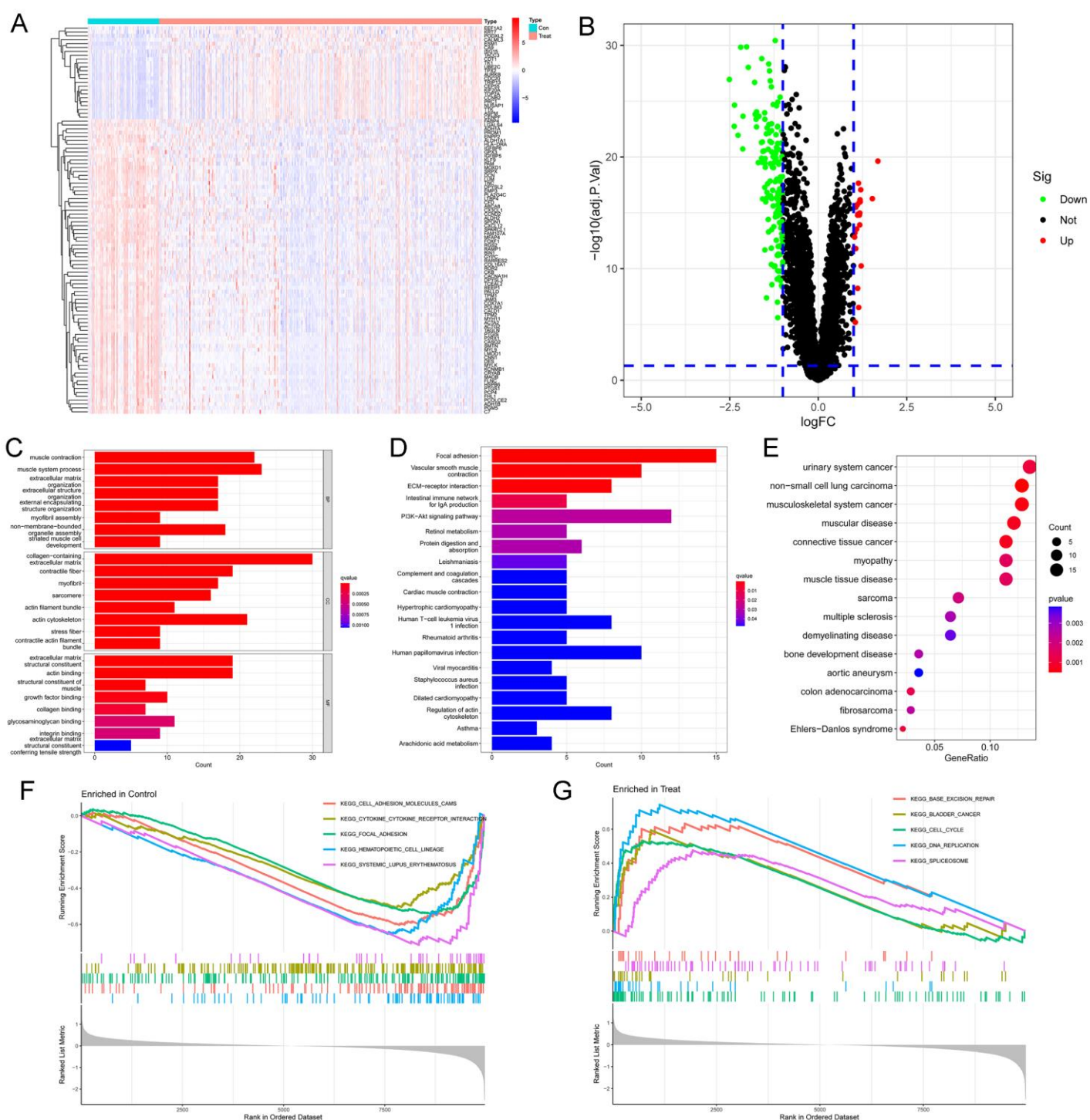


Figure S1. DEGs and their enrichment analysis. (A, B) The volcano plot for 172 DEGs and the heat map for most relevant 100 DEGs (24 upregulated and 148 down-regulated). (C, D) Bar plot of GO and KEGG analyses for DEGs. (E) Bubble plot of DO analysis for DEGs. (F, G) GSEA analysis in BC and normal samples. DEG: differentially expressed genes; GO: Gene ontology; KEGG: Kyoto Encyclopedia of Genes and Genomes; DO: Disease ontology; GSEA: Gene Set Enrichment Analysis.

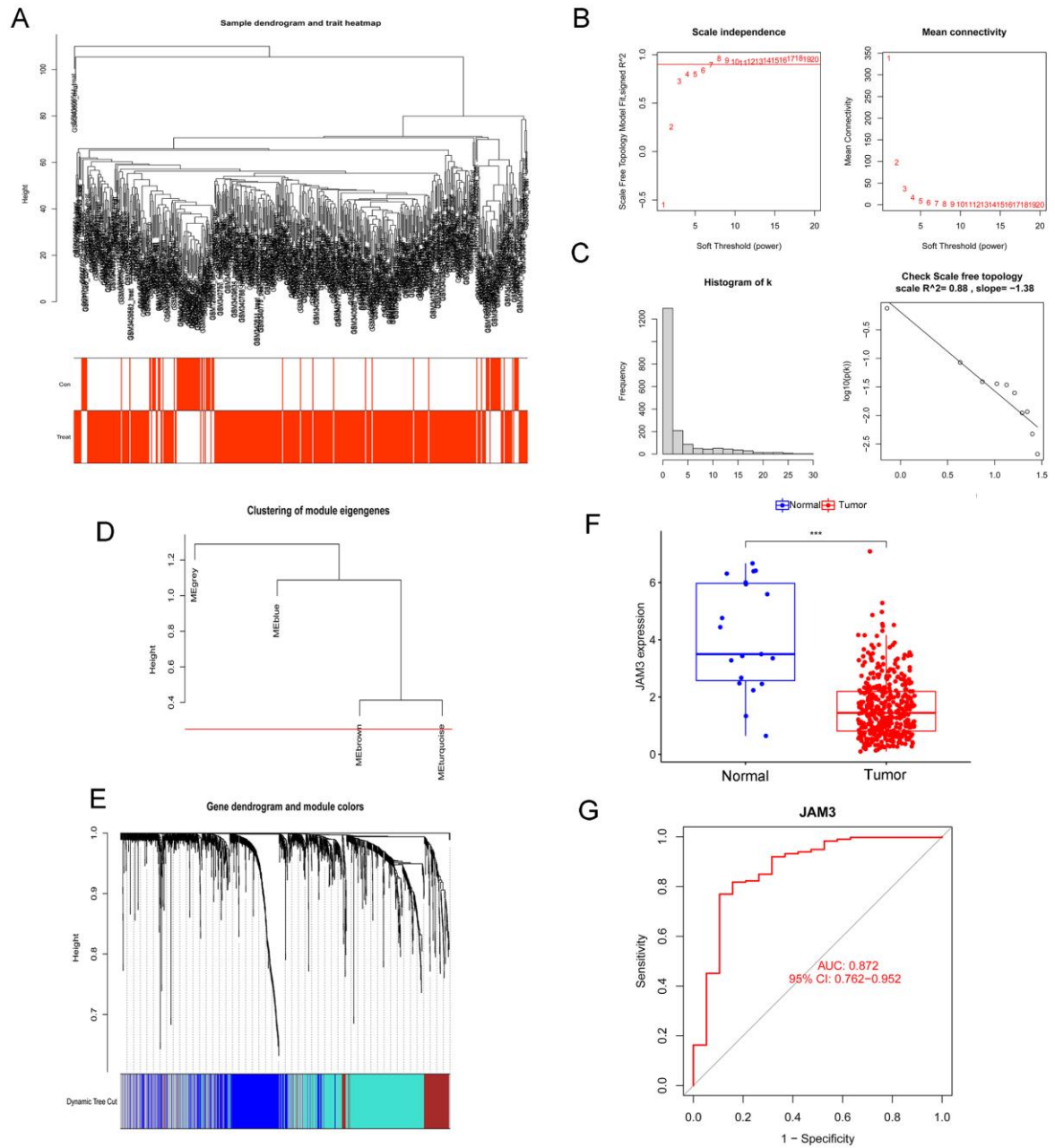


Figure S2. Construction of BC-related gene co-expression modules. (A) Clustering dendrogram and trait indicator of 481 samples. (B) Analysis of the scale-free fit index and the mean connectivity for various soft - thresholding powers. (C) Scale free topology when the power value was seven. (D) Hierarchical clustering analysis of WGCNA modules. (E) Dendrogram of all genes clustered based on a dissimilarity measure (1 - TOM). (F) Boxplot of JAM3 expression across BC and normal samples in TCGA cohort. (G) ROC curve of JAM3 as a diagnostic gene for BC in the TCGA cohort. WGCNA: weighted correlation network analysis; JAM3: Junctional adhesion molecule 3; BC: Bladder cancer; TGCA: The Cancer Genome Atlas.

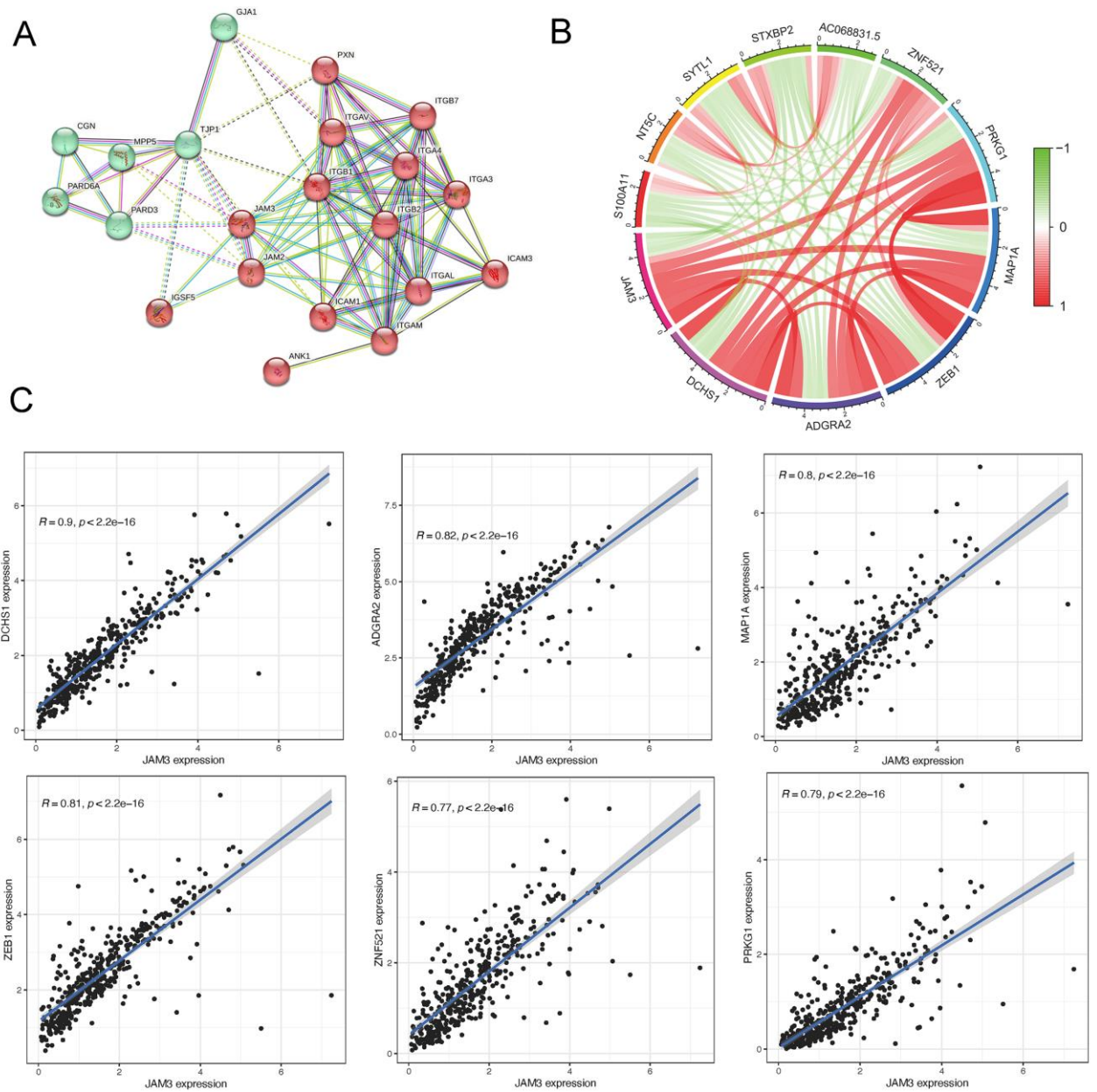
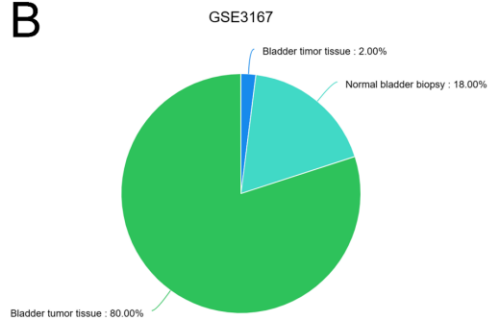


Figure S3. Co-expression network of JAM3 in BC. (A) Protein-protein interaction network for JAM3. (B) The top five genes negatively correlated with JAM3 and the top six genes positively correlated with JAM3. (C) The top six strongest positively co-expressed genes.

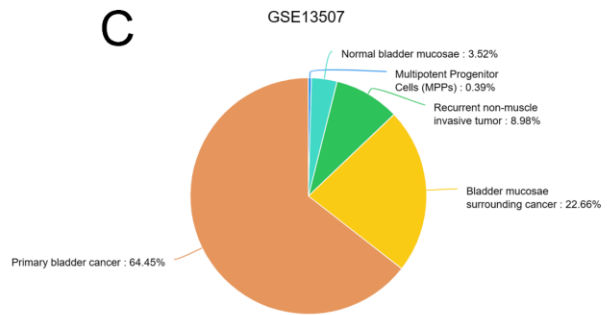
A

GEO Series	Sample source	Frequency	Percentage(%)	umulative percentage(%)
GSE3167(n=50)	Bladder tumor tissue	1	2	2
	Bladder tumor tissue	40	80	82
	Normal bladder biopsy	9	18	100
GSE13507(n=265)	Bladder mucosae surrounding cancer	58	22.66	22.66
	Multipotent Progenitor Cells (MPPs)	1	0.39	23.05
	Normal bladder mucosae	9	3.52	26.56
	Primary bladder cancer	165	64.45	91.02
	Recurrent non-muscle invasive tumor	23	8.98	100
GSE52519(n=12)	Bladder cancer tissue	9	75	75
	Bladder healthy tissue	3	25	100
GSE65635(n=12)	Bladder cancer	8	66.67	66.67
	Normal bladder mucosa	2	16.67	83.33
	Pooled normal bladder mucosa samples	2	16.67	100
GSE100926(n=6)	Mucle invasive Bladder_cancer_tissue_patient1	1	16.67	16.67
	Mucle invasive Bladder_cancer_tissue_patient2	1	16.67	33.33
	Mucle invasive Bladder_cancer_tissue_patient3	1	16.67	50
	Normal_adjacent_tissue_patient1	1	16.67	66.67
	Normal_adjacent_tissue_patient2	1	16.67	83.33
	Normal_adjacent_tissue_patient3	1	16.67	100
GSE120736(n=145)	Primary bladder cancer	118	81.38	81.38
	Recurrent bladder tumor	27	18.62	100

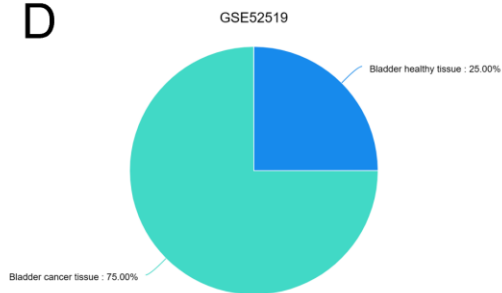
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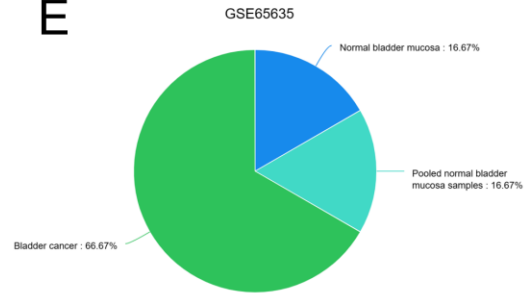
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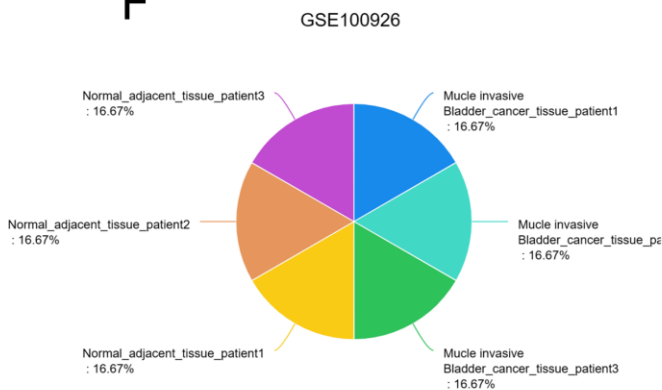
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E



F



G

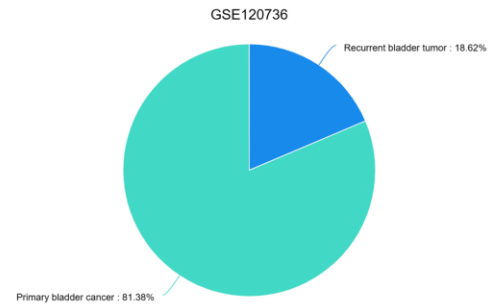


Figure S4. Demonstration of clinical traits in the GEO datasets (GSE3167, GSE13507, GSE52519, GSE65635, GSE100926, GSE120736).

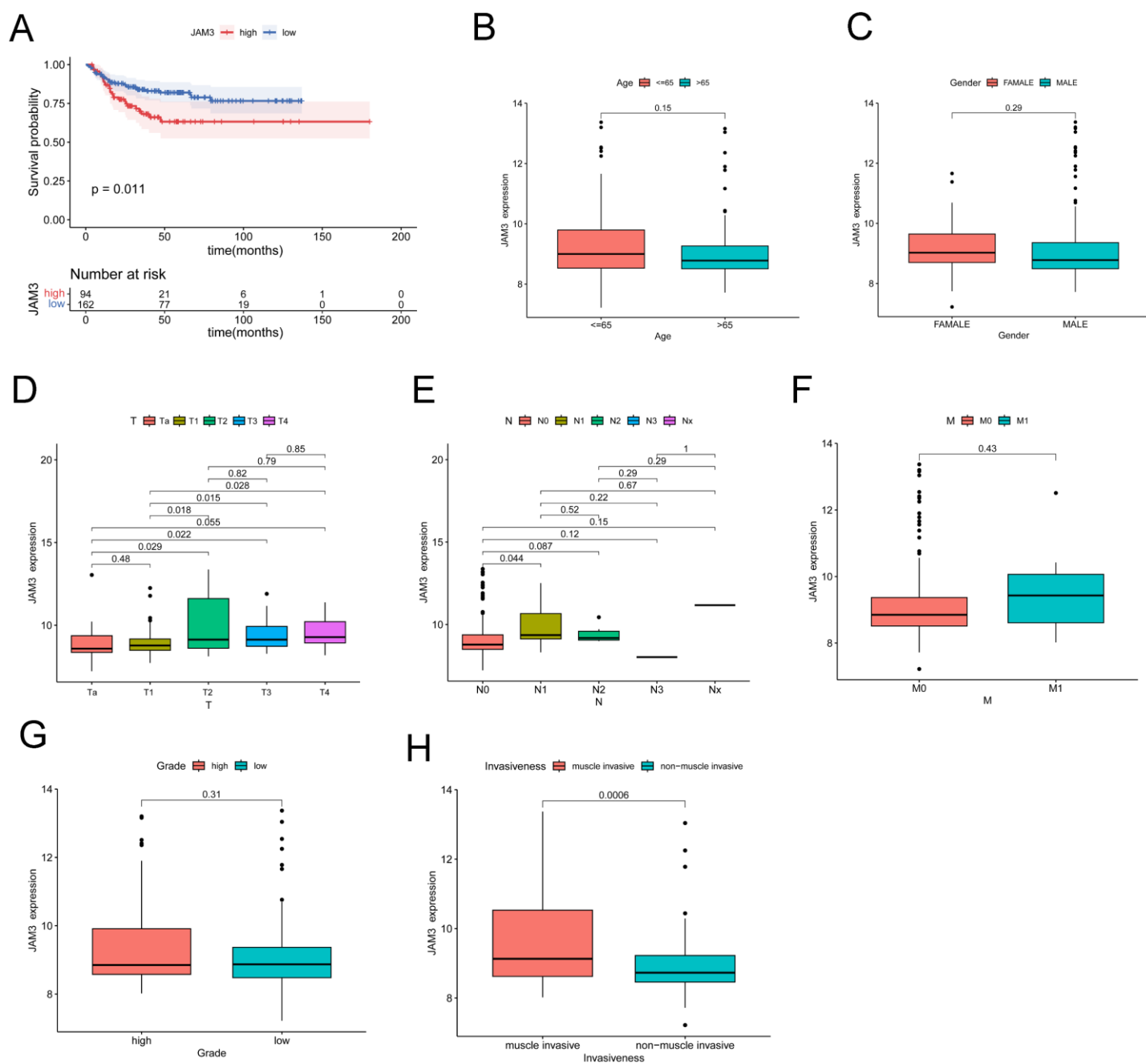


Figure S5. (A) Kaplan-Meier analysis of JAM3 in BC based on GSE13507, GSE48276, GSE37817. (B-H) Relationship between JAM3 expression level and clinical parameters based on GSE13507, GSE48276, GSE37817.

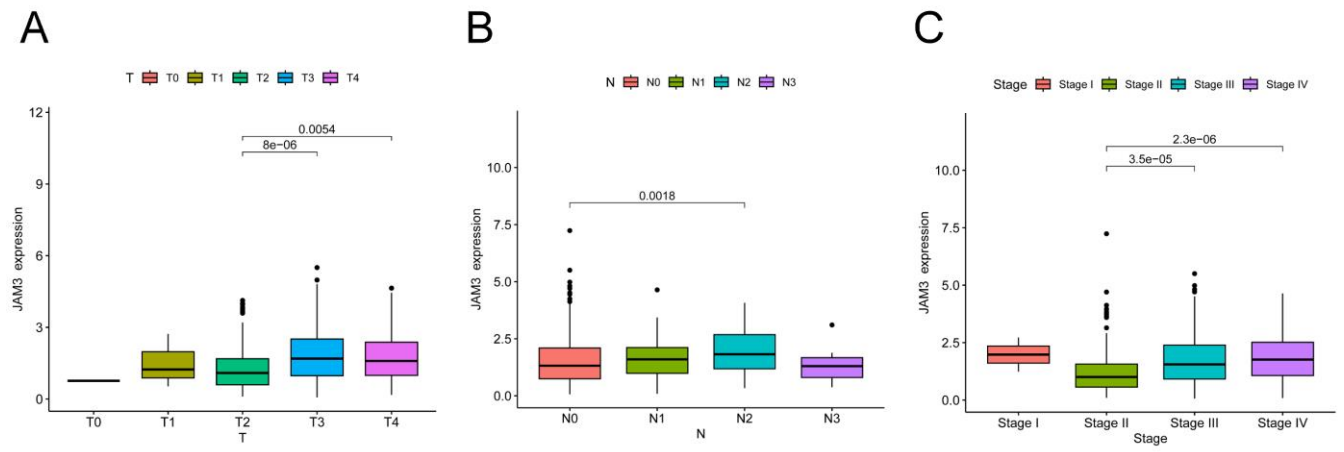


Figure S6. (A-C) Relationship between JAM3 expression level and clinical parameters based on TCGA.

Table S1. Clinical data on patients with bladder cancer from TCGA.

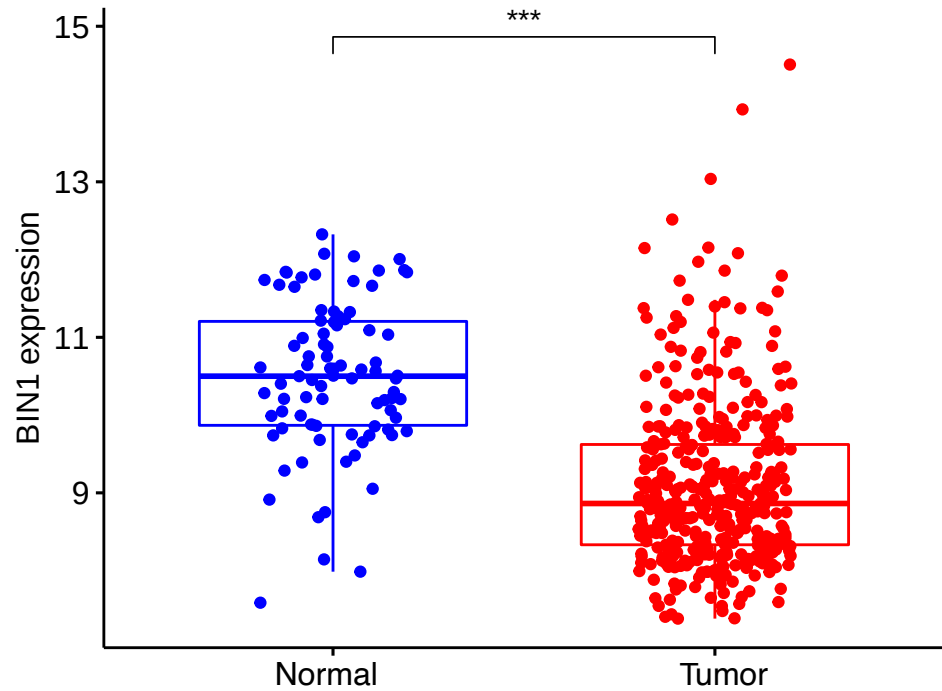
Type	Group	Frequency	Percentage (%)	Cumulative percentage (%)
Age	<65	151	36.65	36.65
	>=65	261	63.35	100.00
Gender	FEMALE	108	26.21	26.21
	MALE	304	73.79	100.00
Grade	High Grade	388	94.17	94.17
	Low Grade	21	5.10	99.27
	unknow	3	0.73	100.00
Stage	Stage I	2	0.49	0.49
	Stage II	131	31.80	32.28
	Stage III	141	34.22	66.50
	Stage IV	136	33.01	99.51
	unknow	2	0.49	100.00
T	T0	1	0.24	0.24
	T1	3	0.73	0.97
	T2	120	29.13	30.10
	T3	196	47.57	77.67
	T4	59	14.32	91.99
	unknow	33	8.01	100.00
M	M0	196	47.57	47.57
	M1	11	2.67	50.24
	unknow	205	49.76	100.00
N	N0	239	58.01	58.01
	N1	47	11.41	69.42
	N2	76	18.45	87.86
	N3	8	1.94	89.81
	unknow	42	10.19	100.00
Total		412	100.0	100.00

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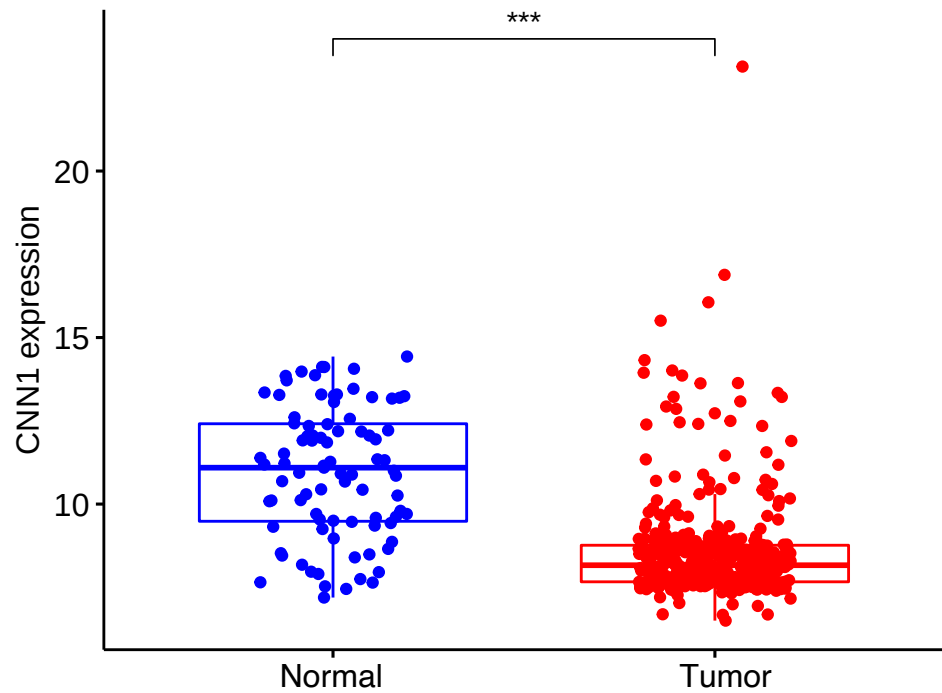
SUPPLEMENTARY MATERIAL 1

Boxplot of 15 genes' expression across BC and normal samples in
GEO cohort

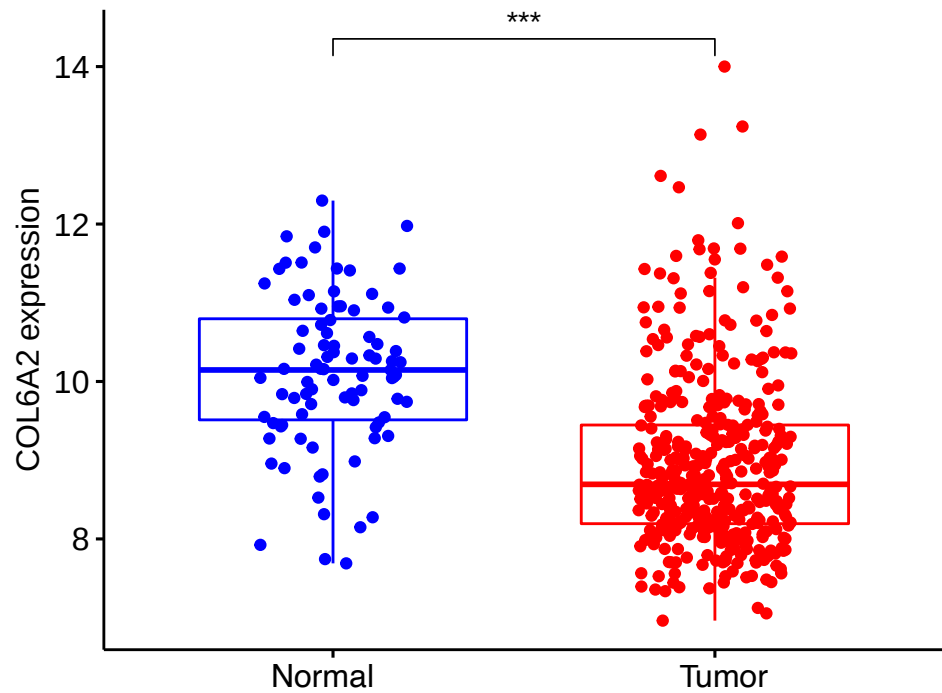
Normal Tumor



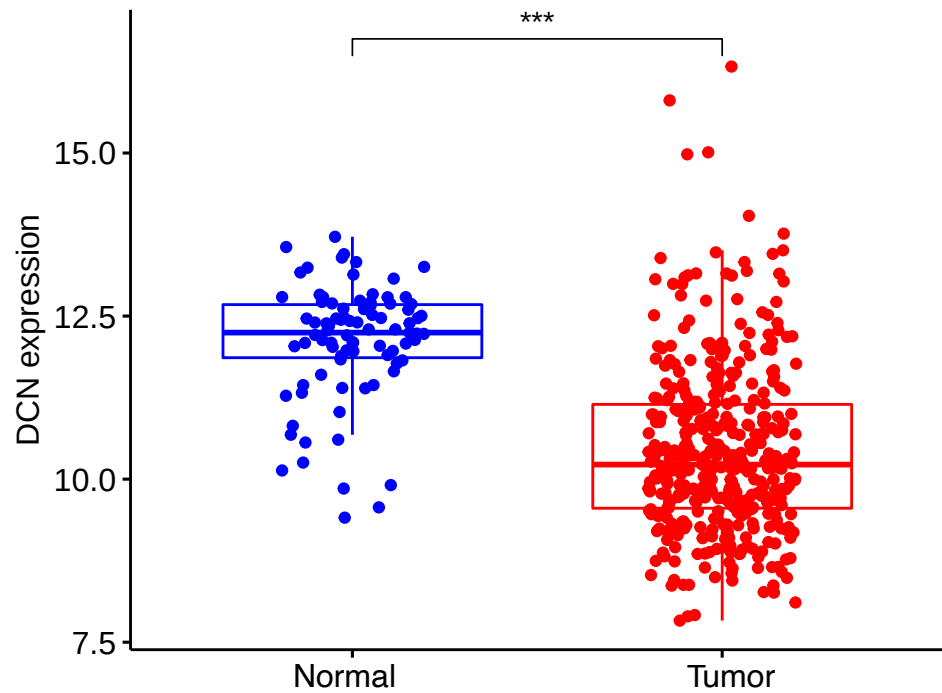
Normal Tumor



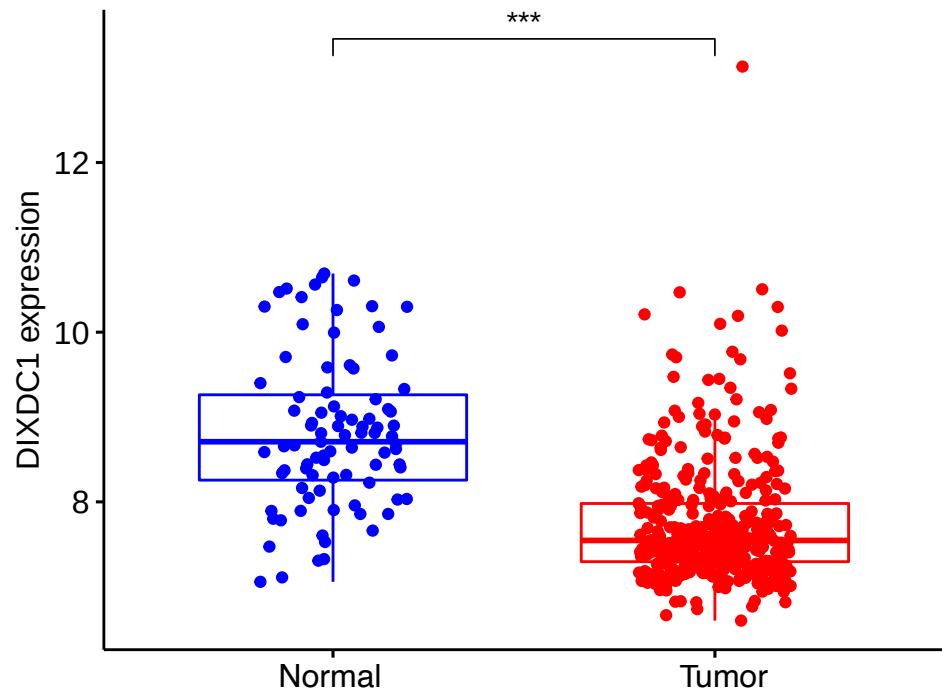
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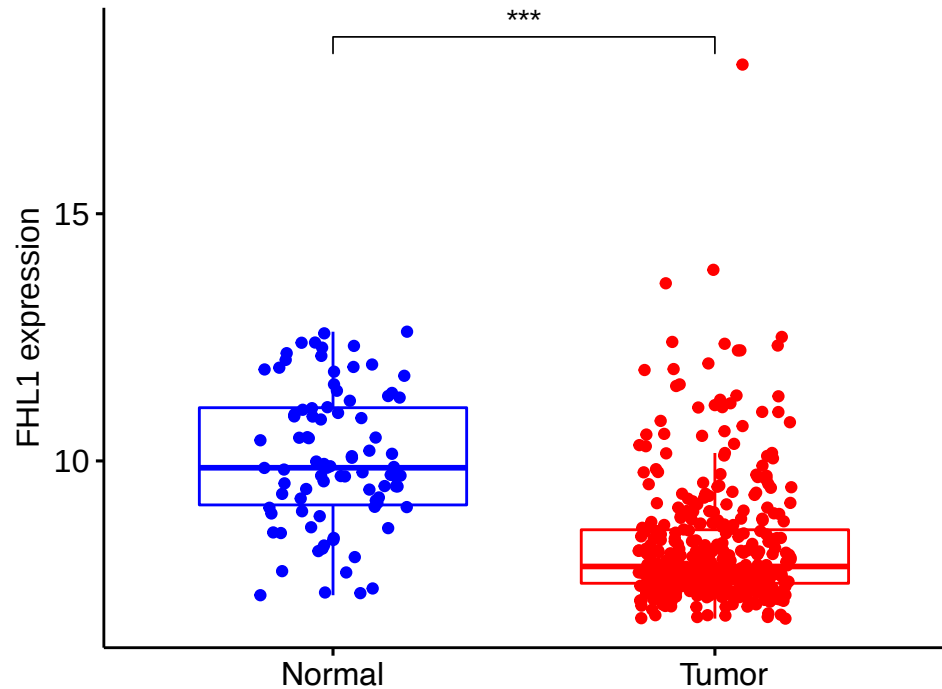
Normal Tumor



Normal Tumor



Normal Tumor



Normal Tumor

FLNC expression

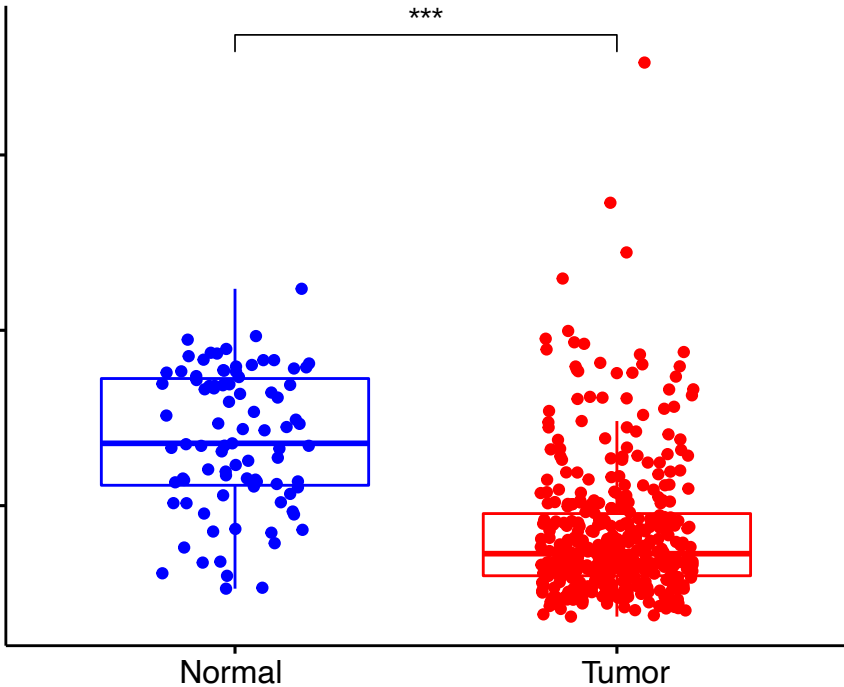
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14

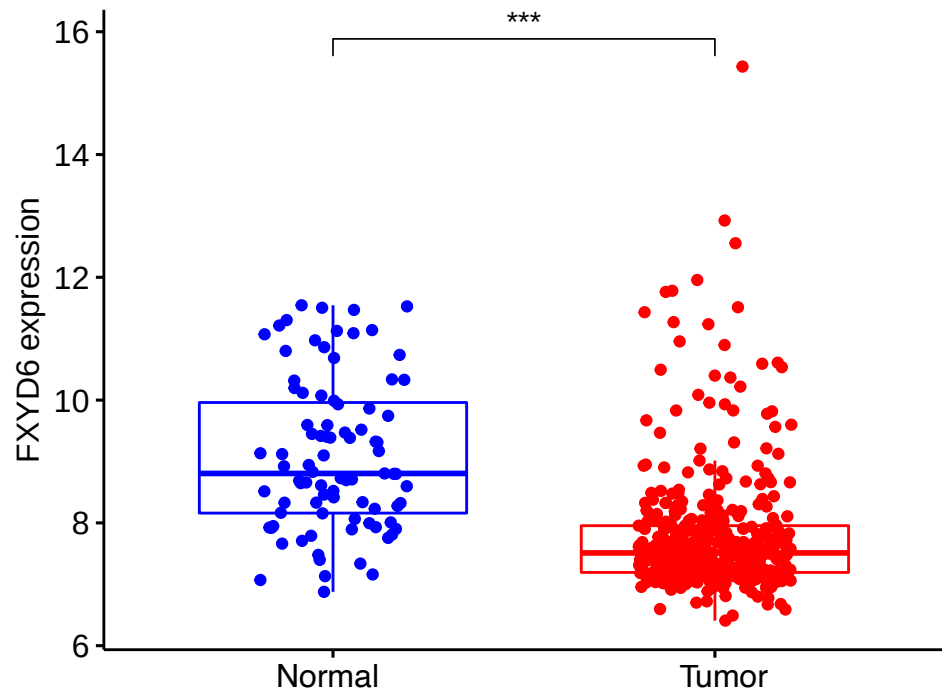
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Normal

Tumor

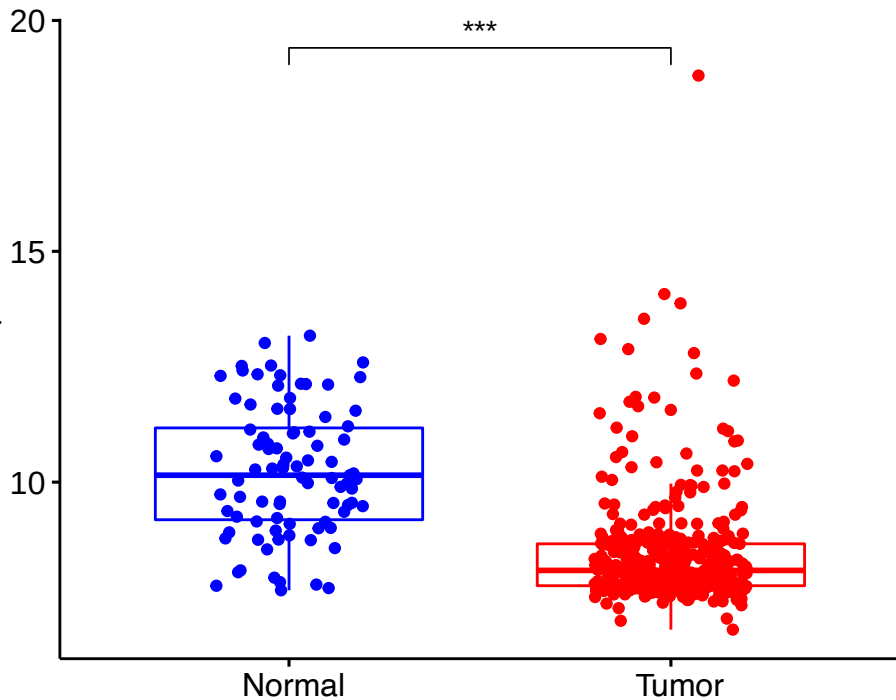


Normal Tumor

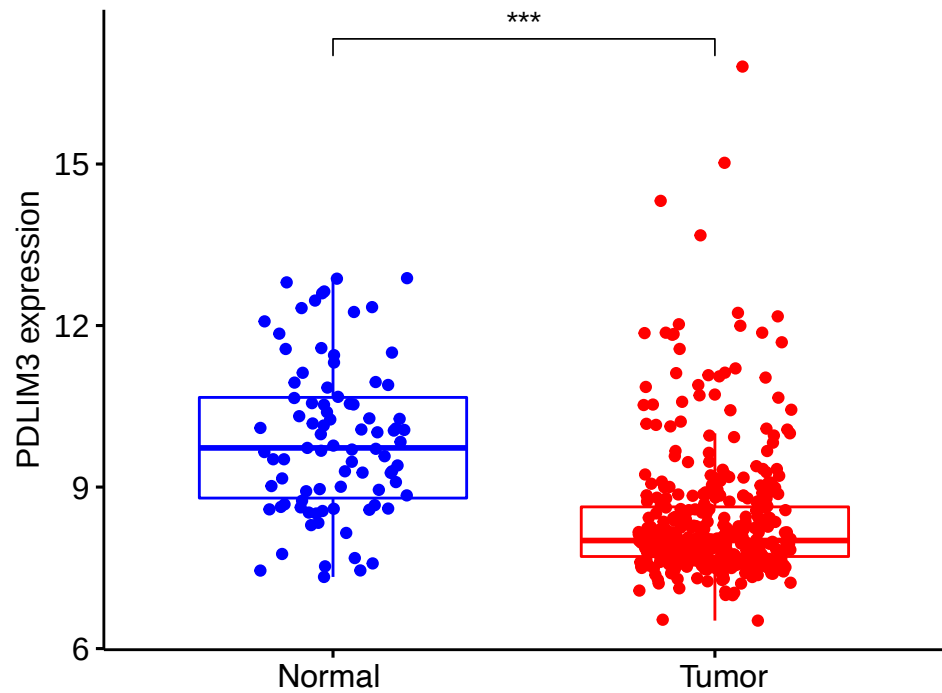


HSPB6 expression

Normal Tumor



Normal Tumor

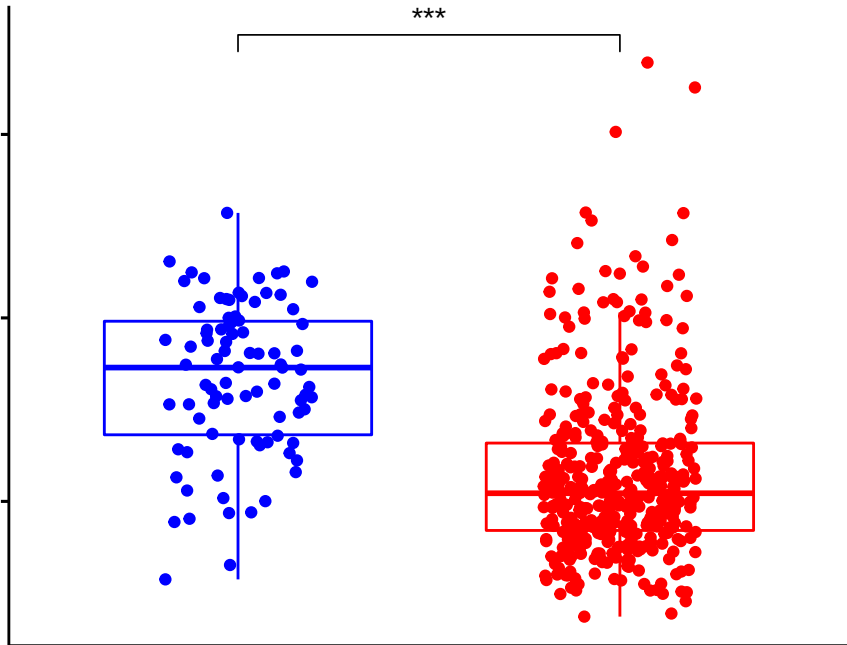


PLA2G4C expression

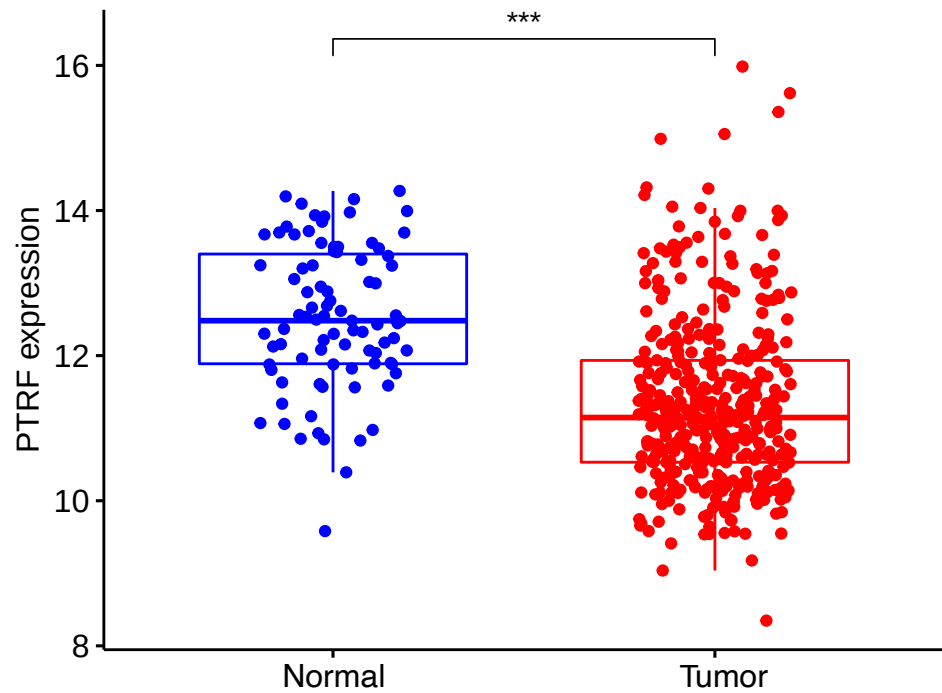
Normal Tumor

Normal

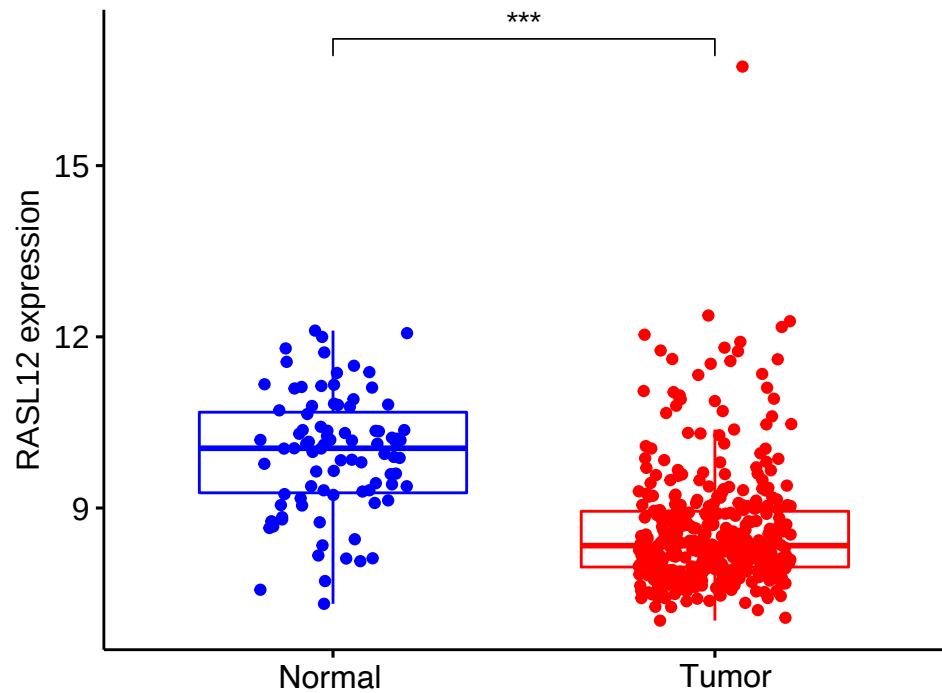
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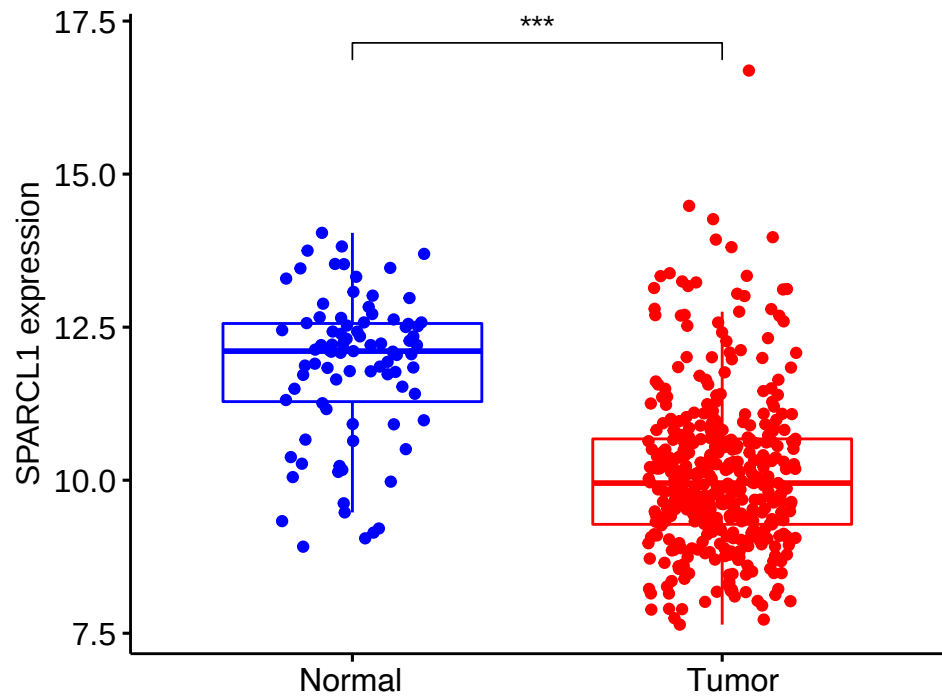
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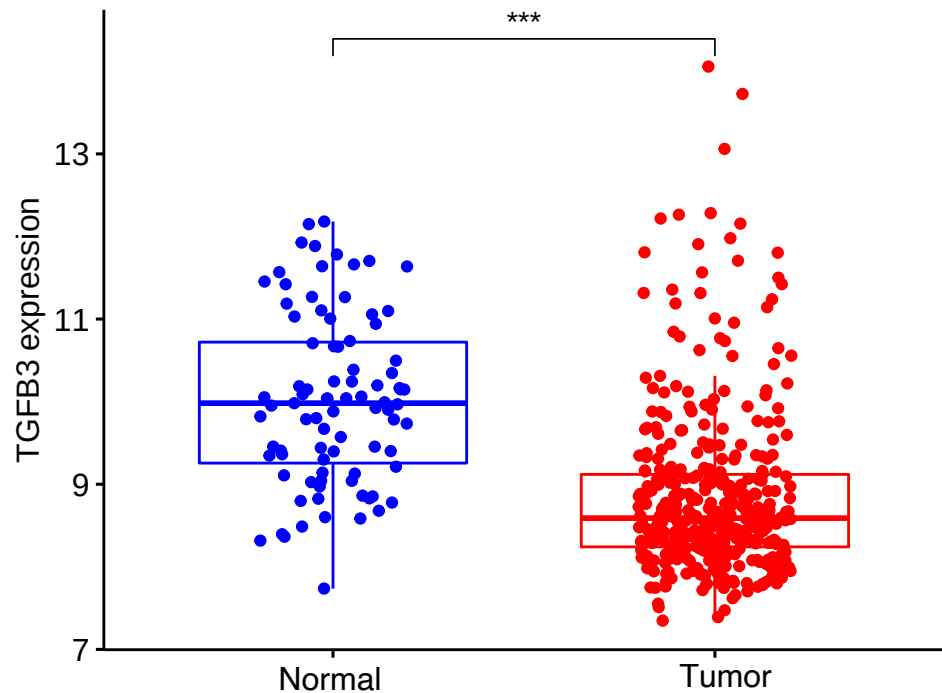
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Normal Tumor



Normal Tumor

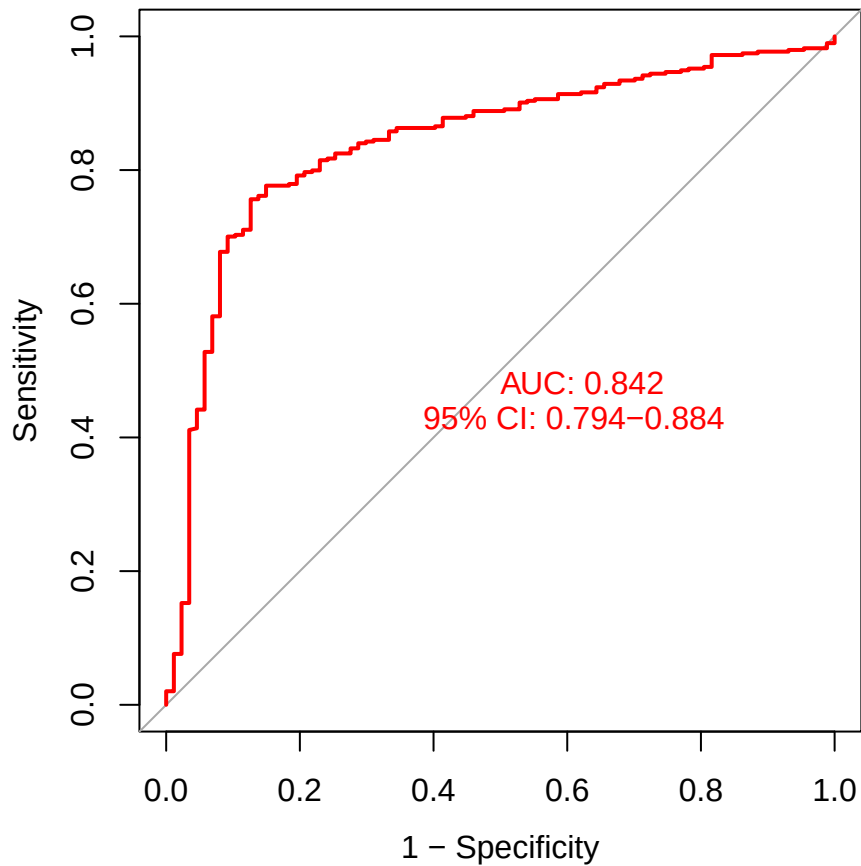


JAM3: A prognostic biomarker for bladder cancer via epithelial-mesenchymal transition regulation

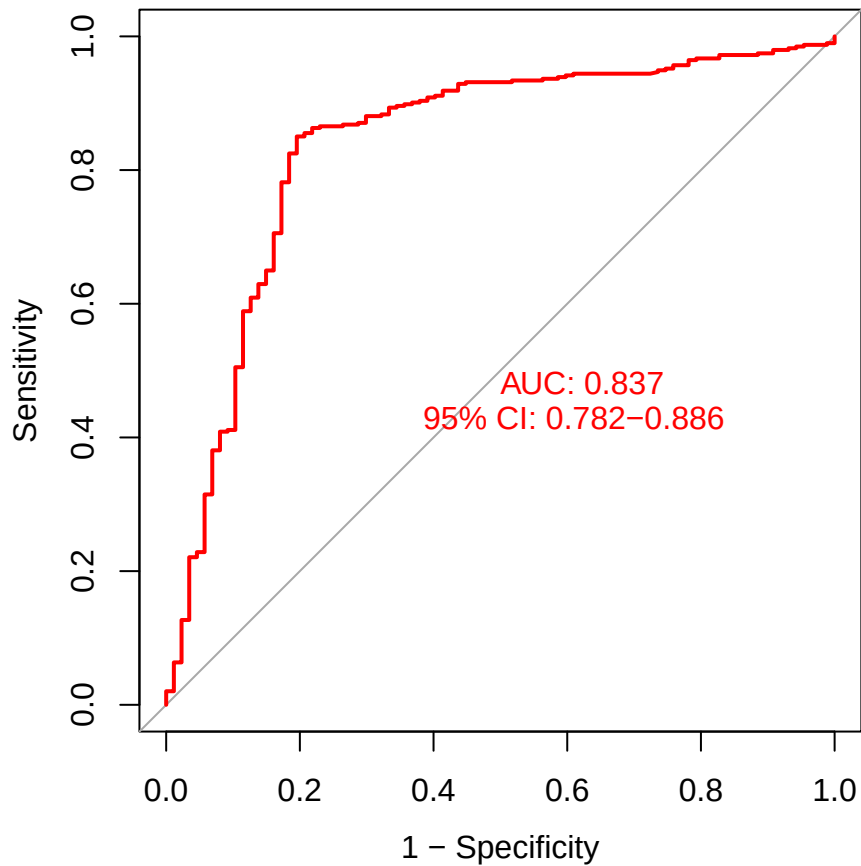
SUPPLEMENTARY MATERIAL 2

ROC curves of 15 genes as the diagnostic genes for BC in GEO cohort

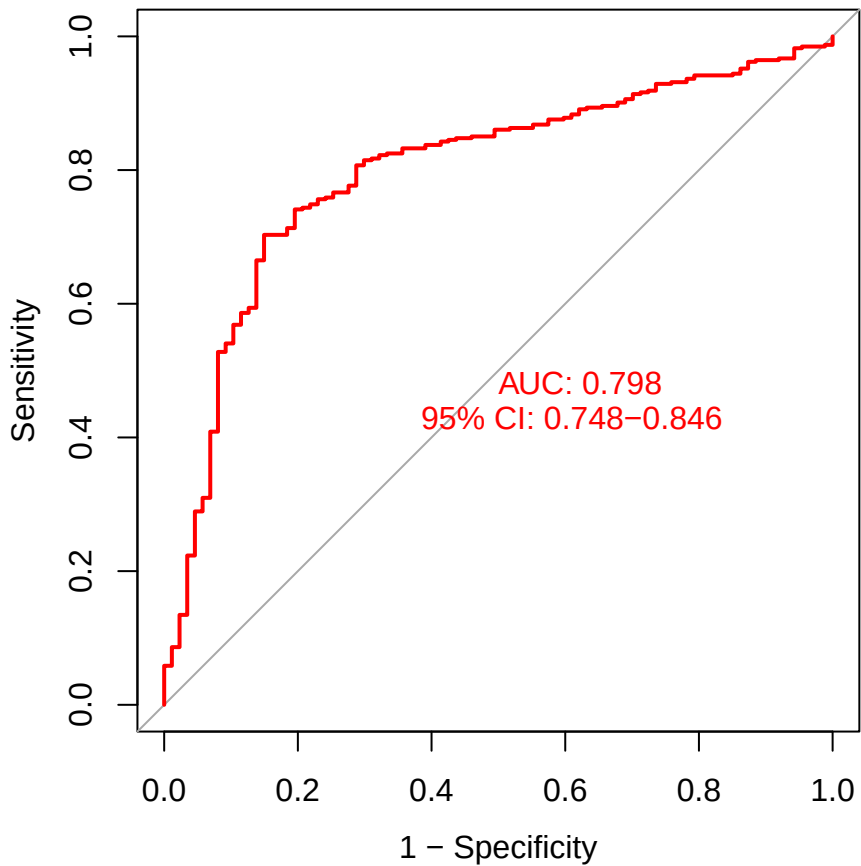
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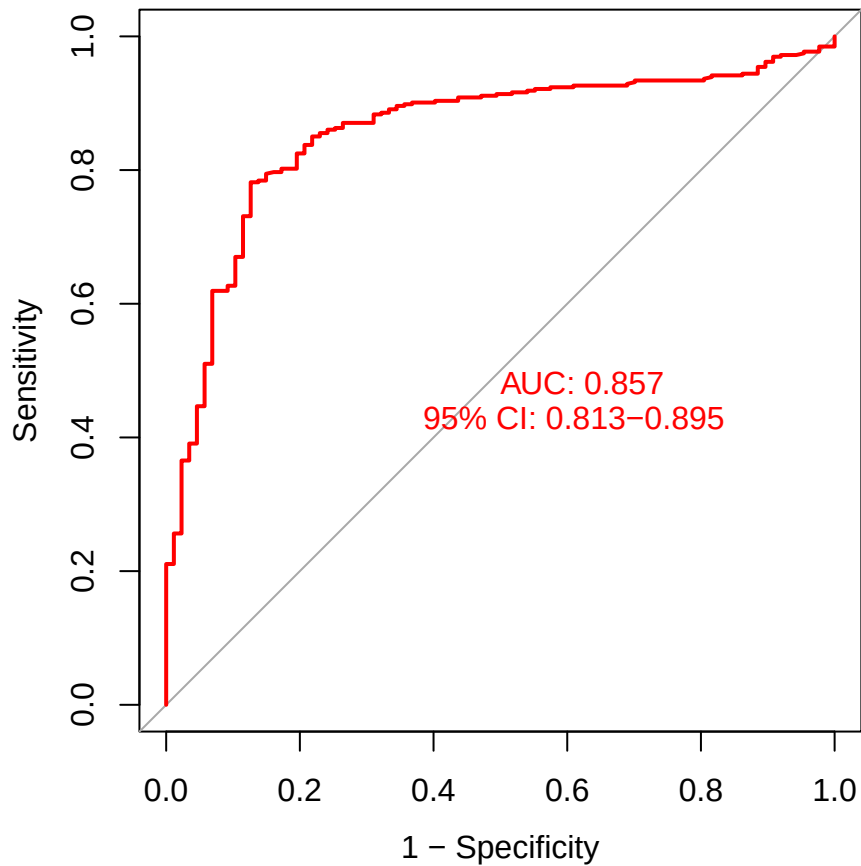
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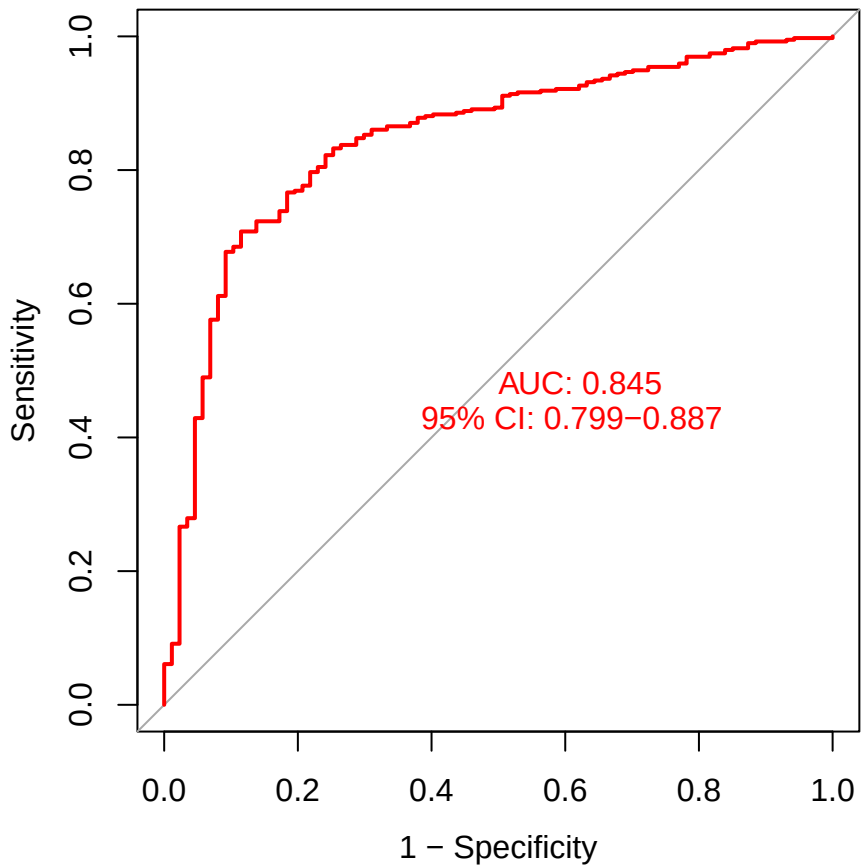
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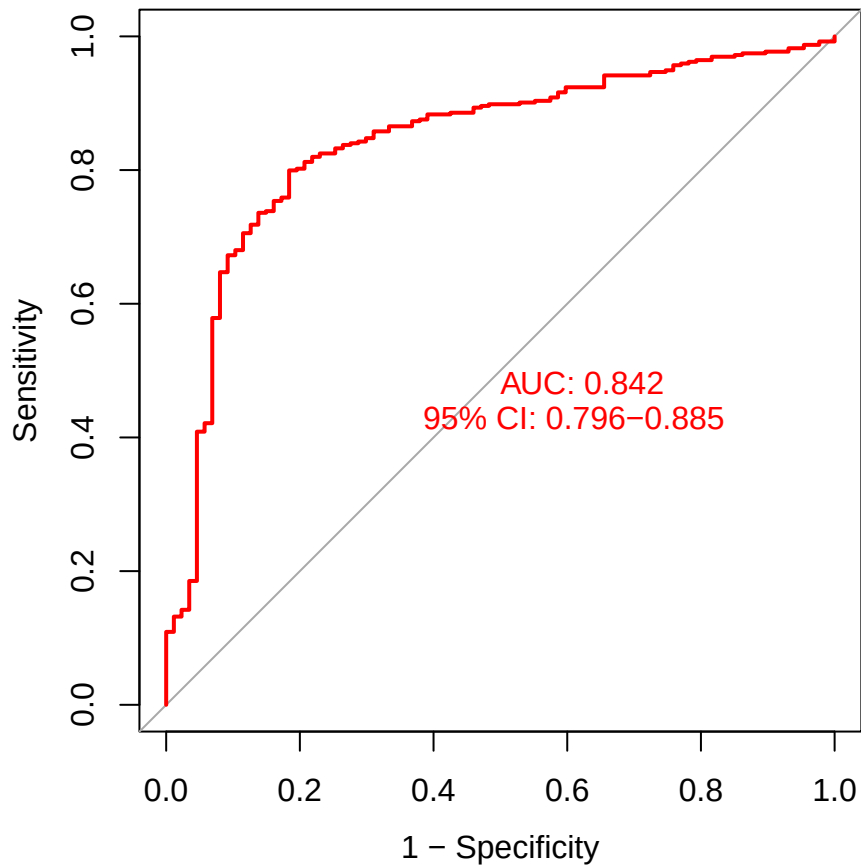
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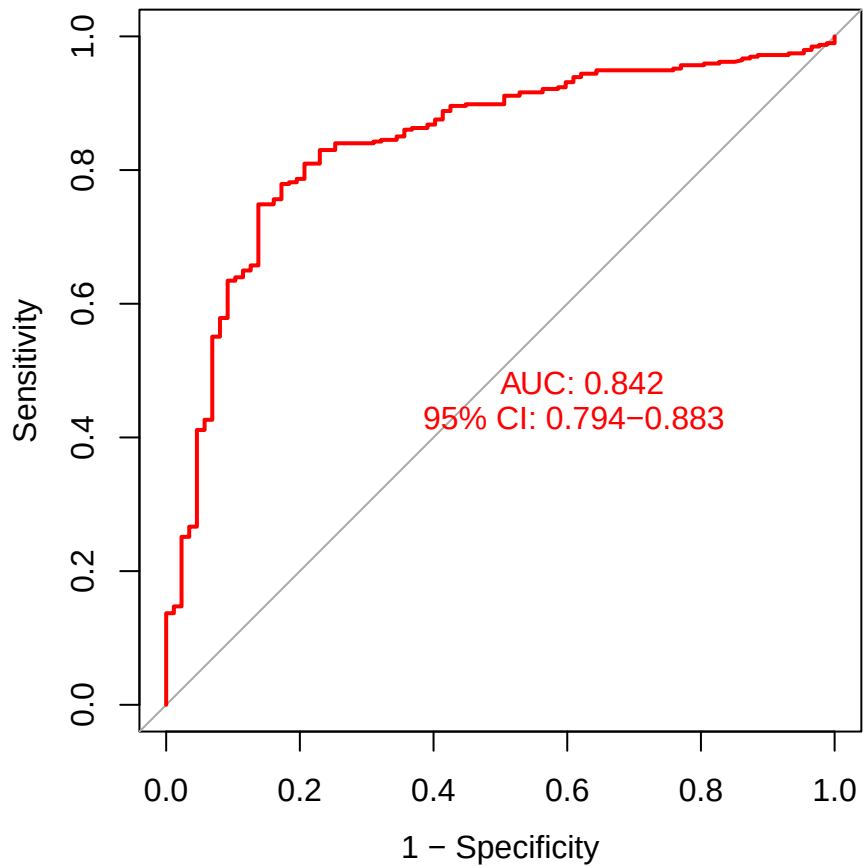
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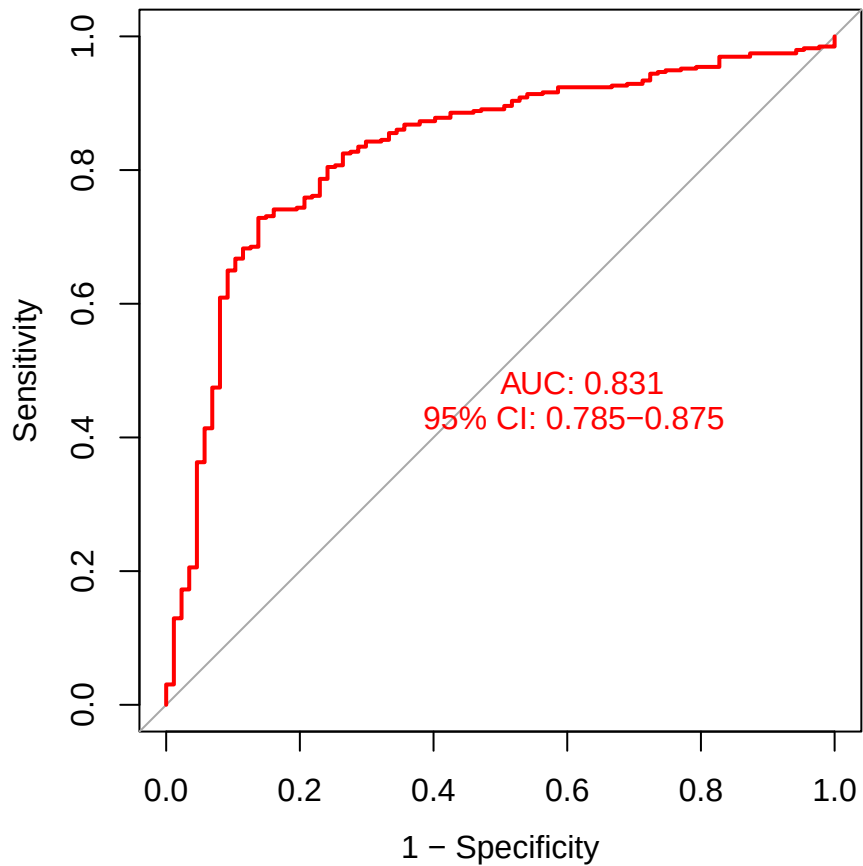
FHL1



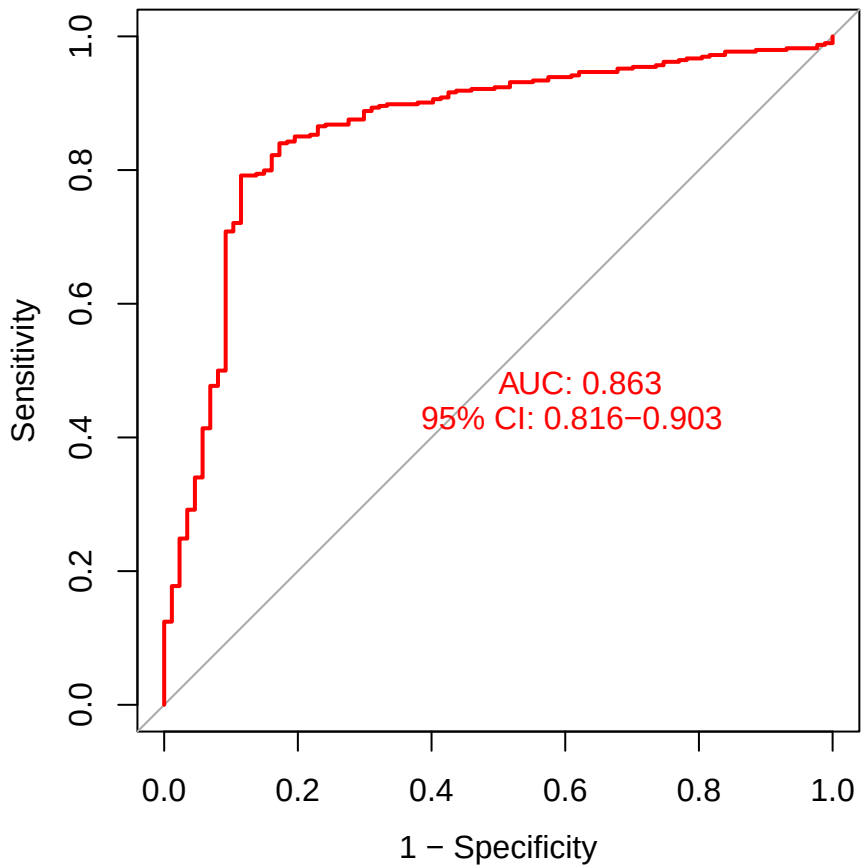
FLNC



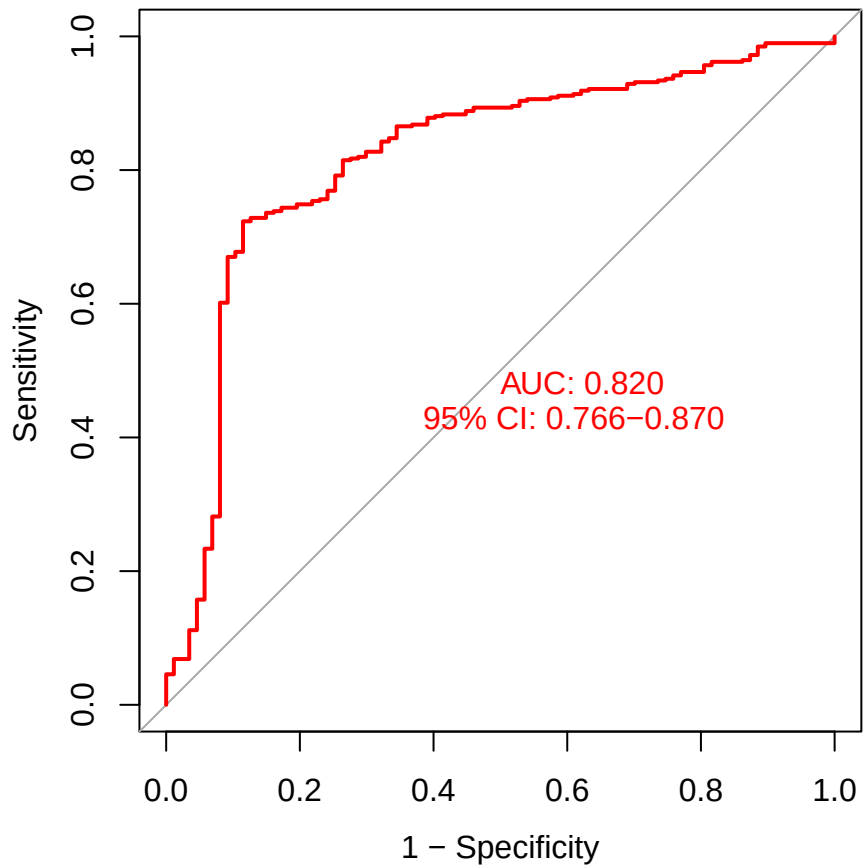
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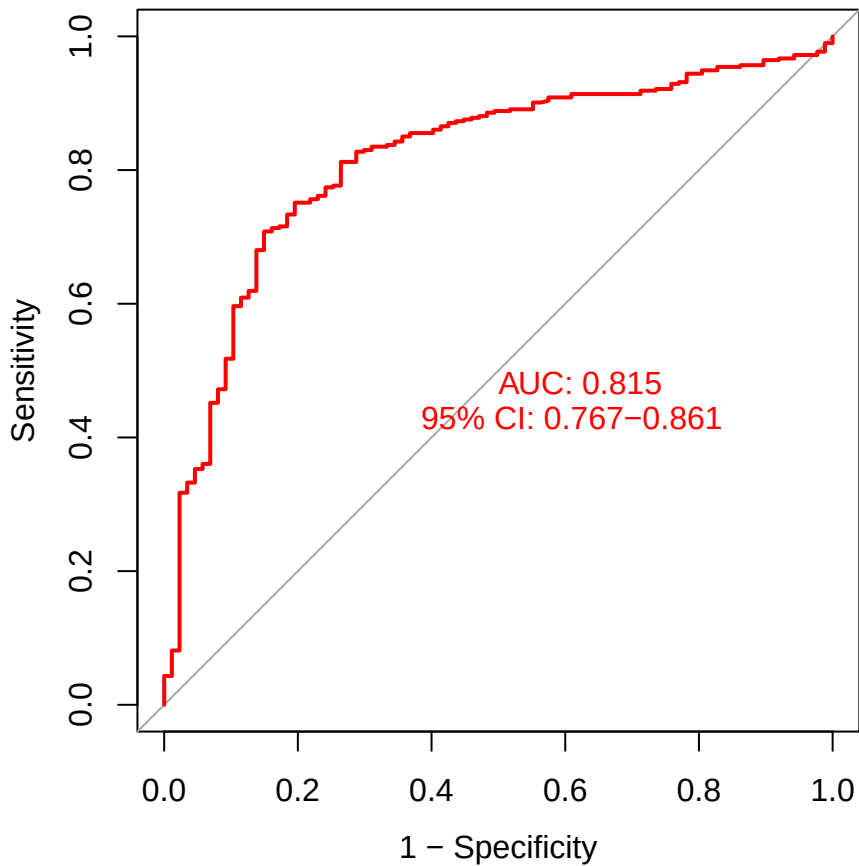
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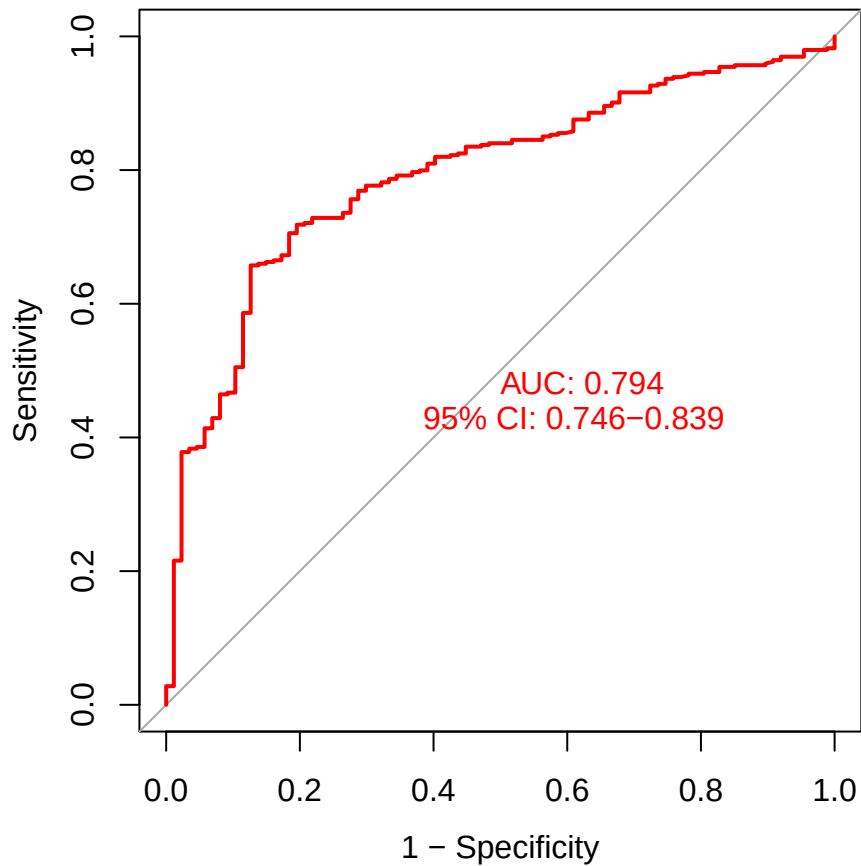
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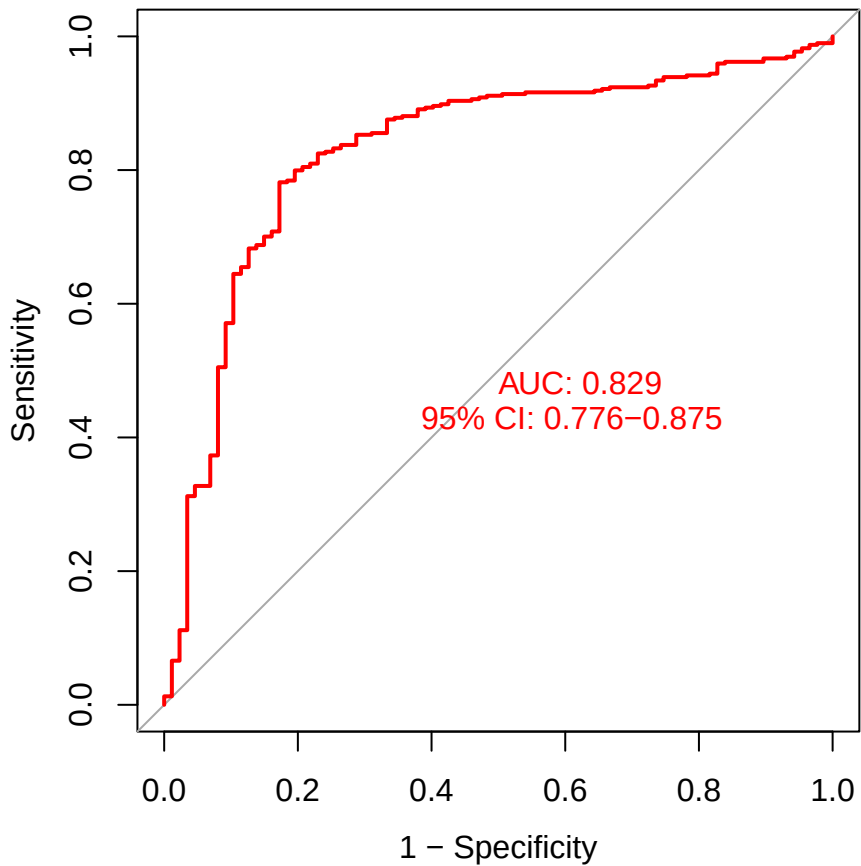
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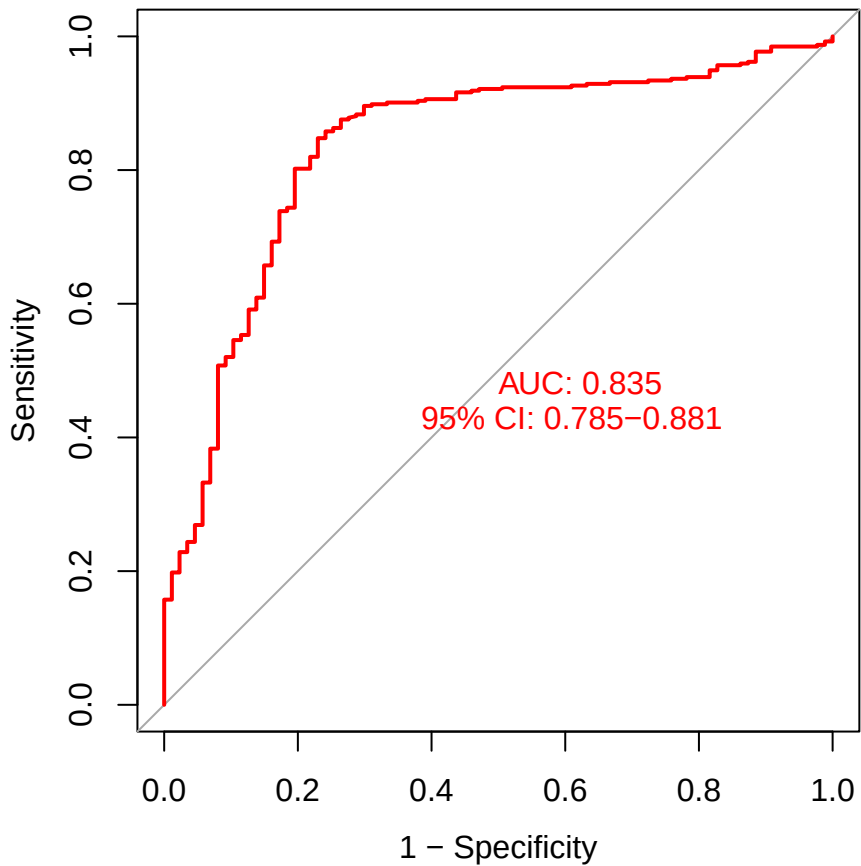
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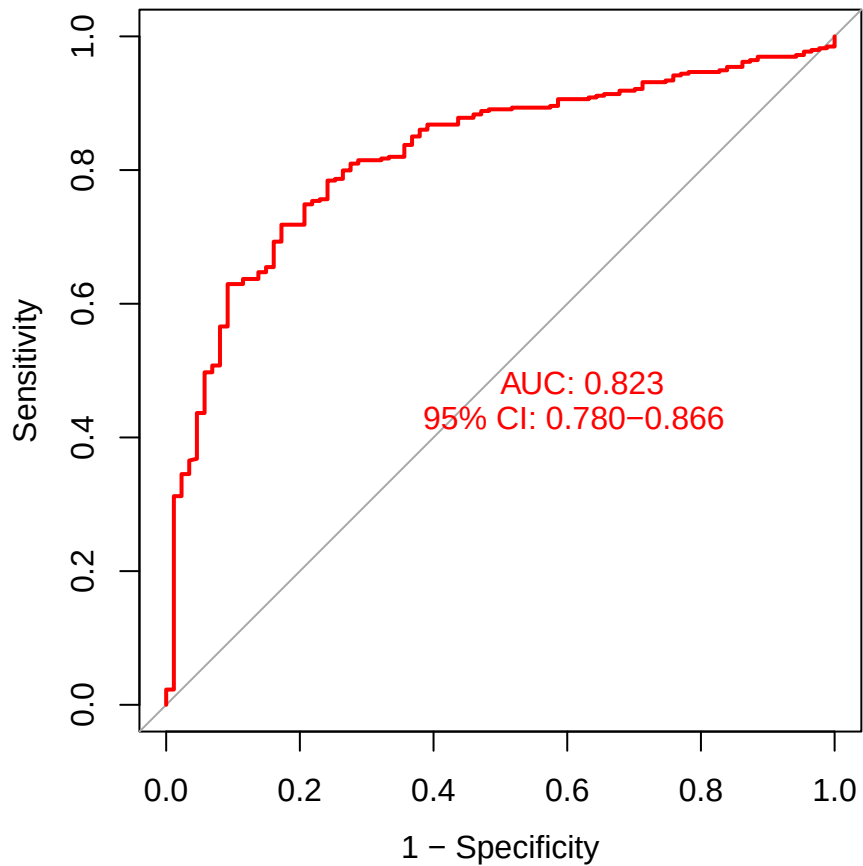
RASL12



SPARCL1



TGFB3

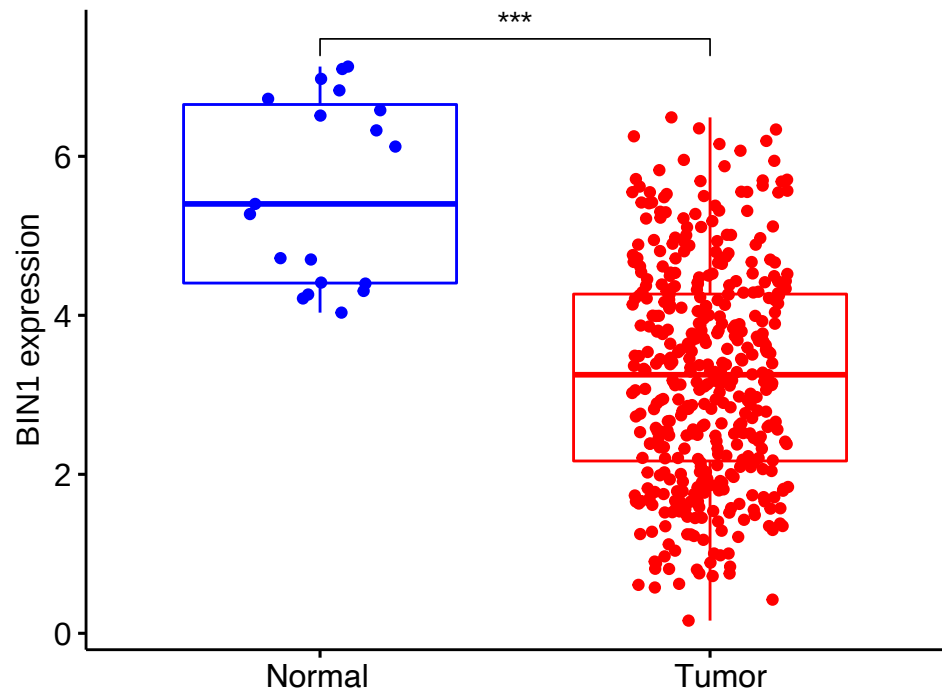


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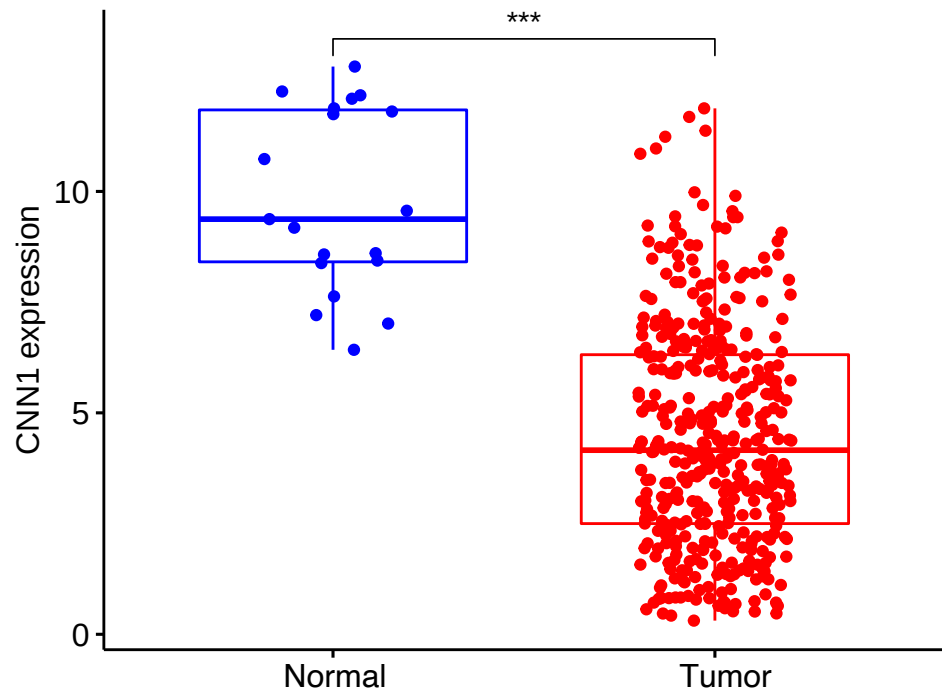
SUPPLEMENTARY MATERIAL 3

Boxplot of 14 genes' expression across BC and normal samples in
TCGA cohort

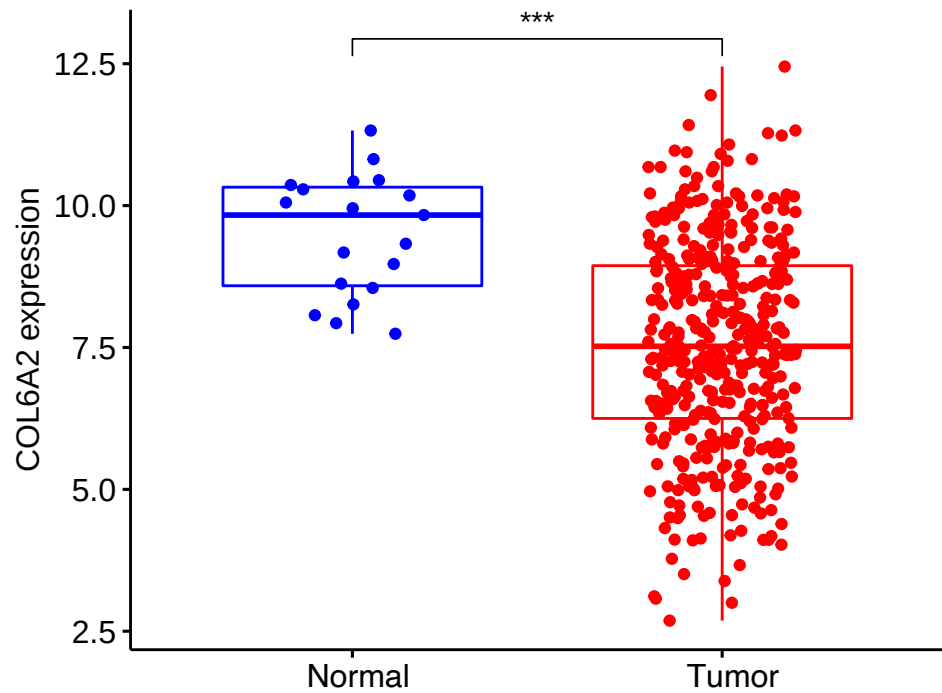
Normal Tumor



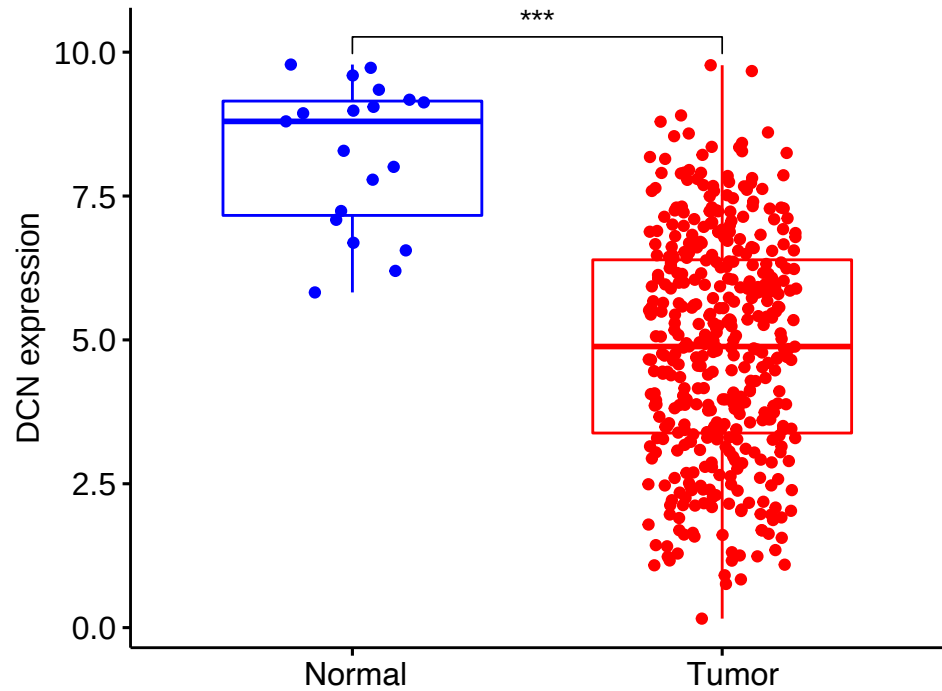
Normal Tumor



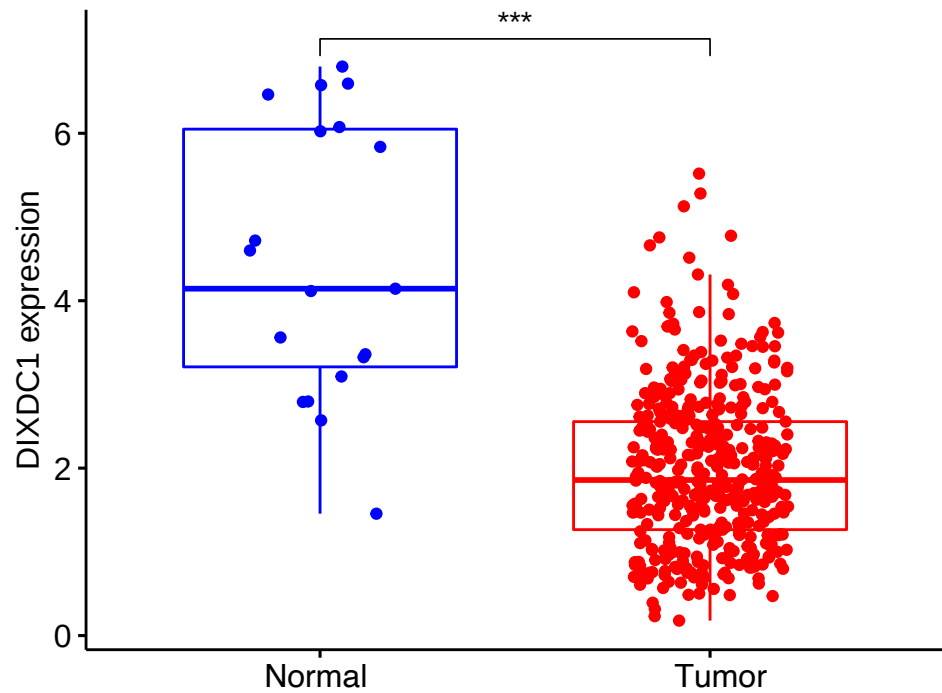
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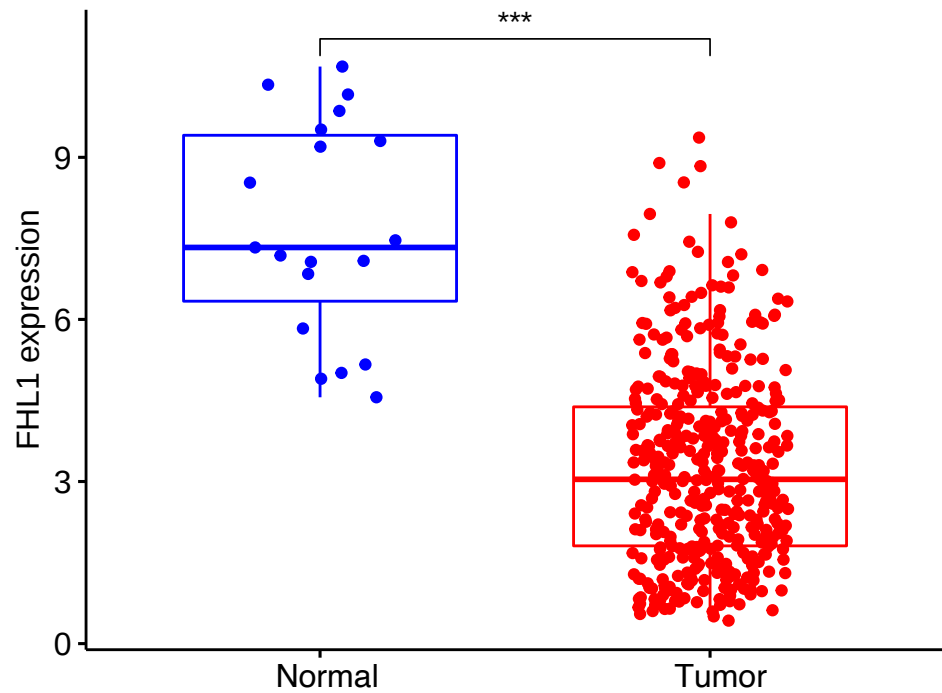
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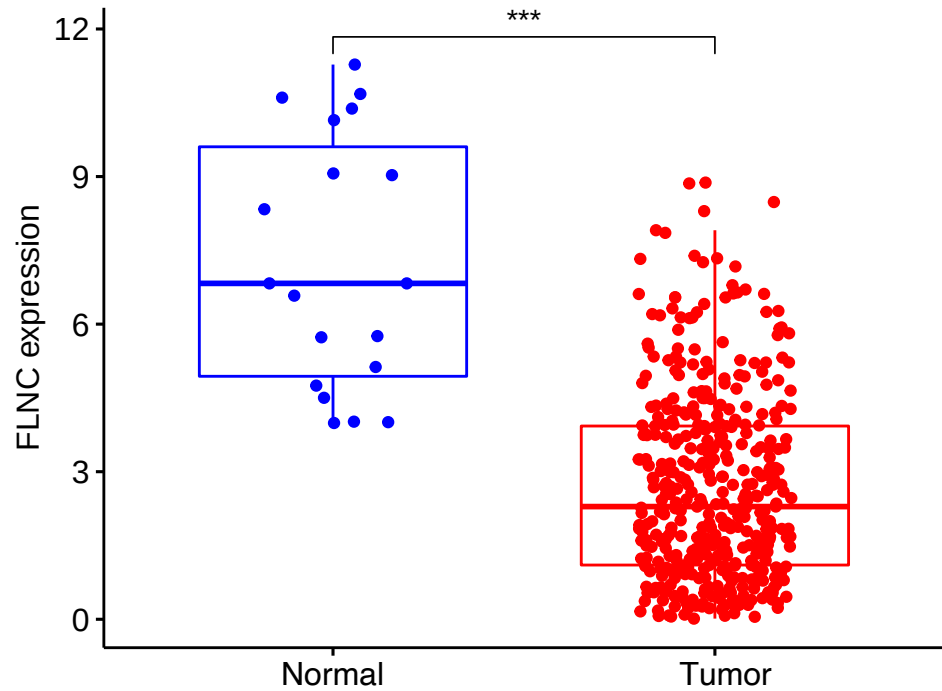
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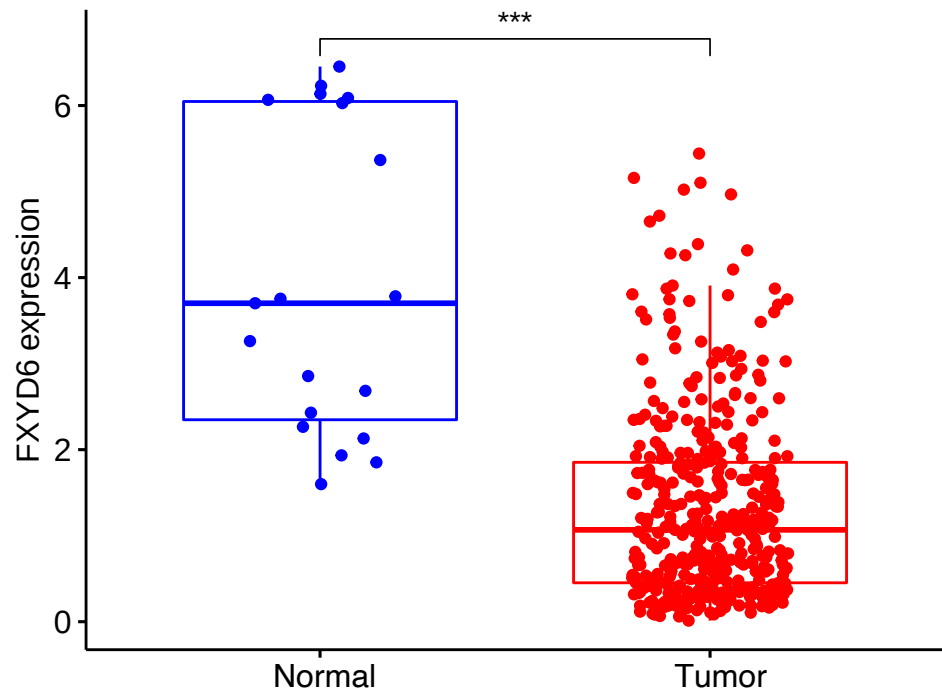
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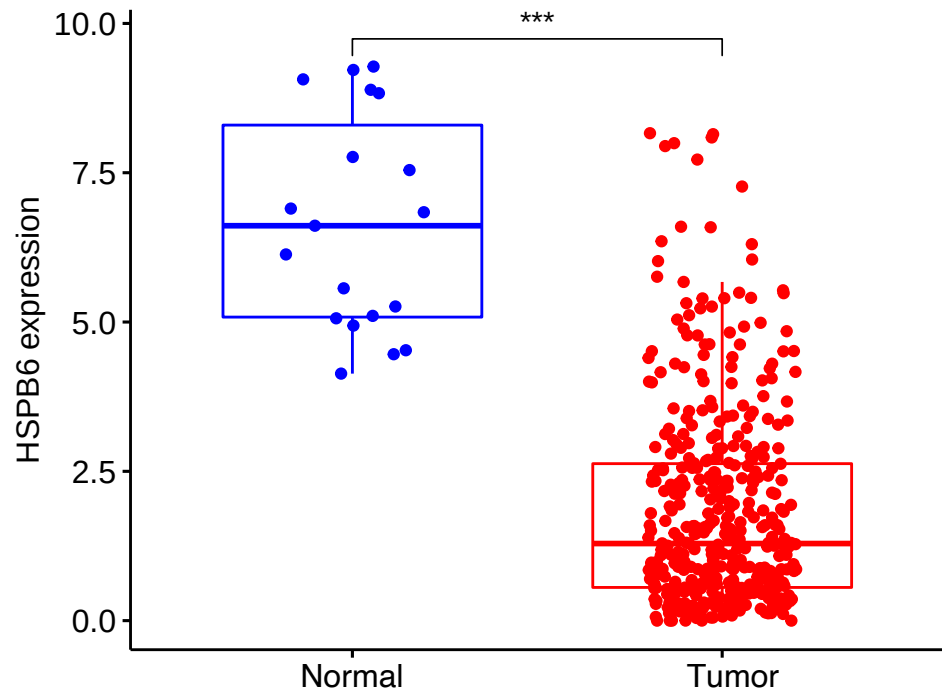
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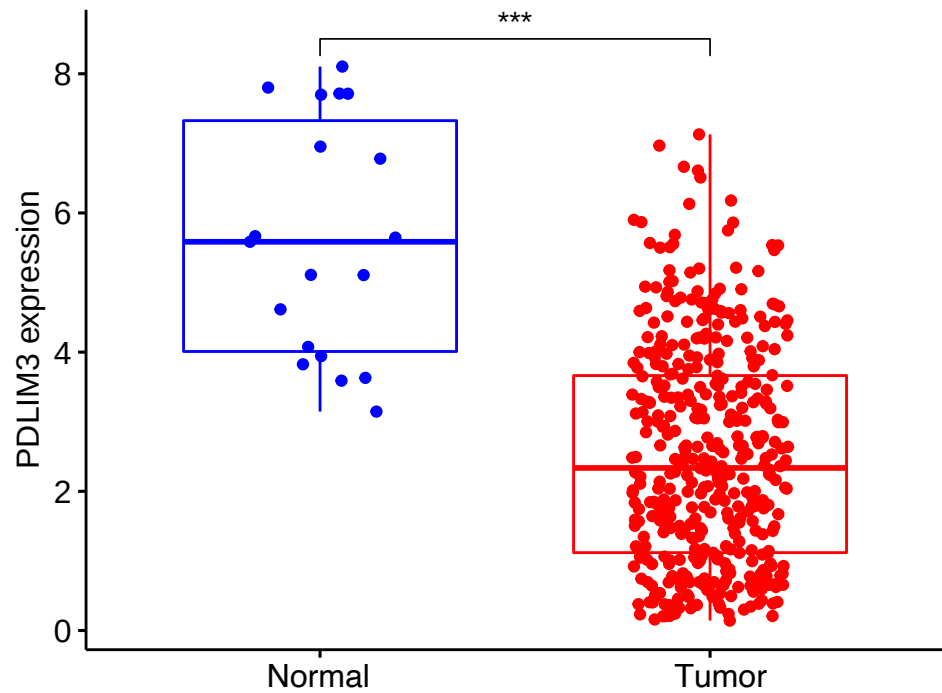
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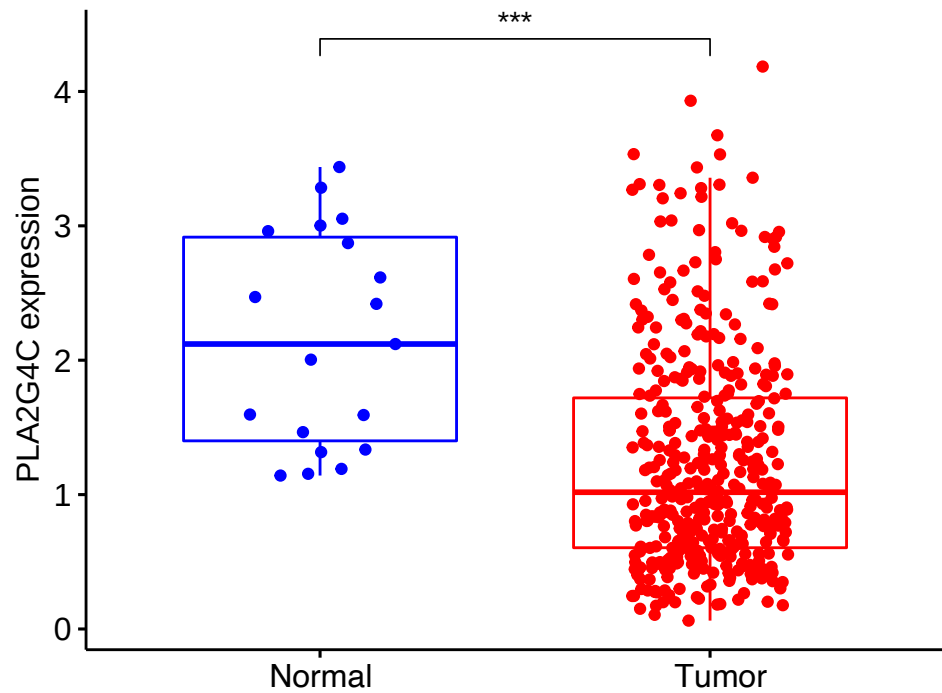
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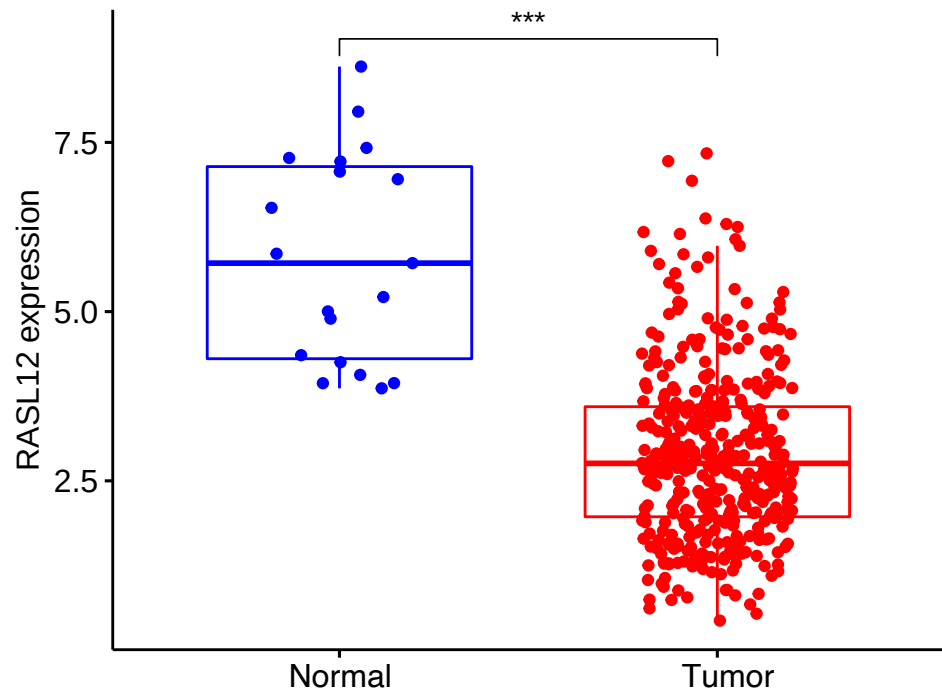
Normal Tumor



Normal Tumor

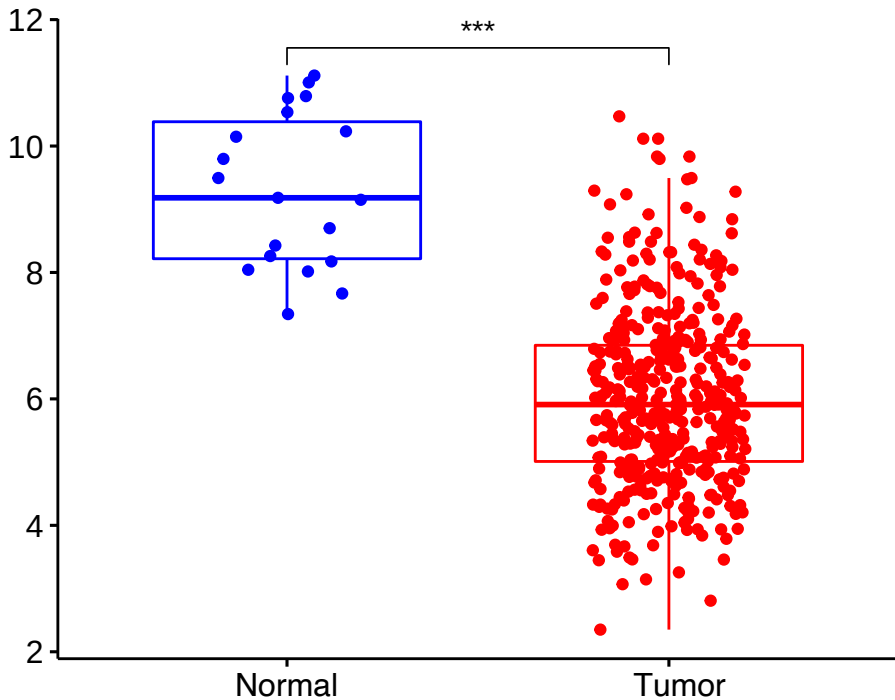


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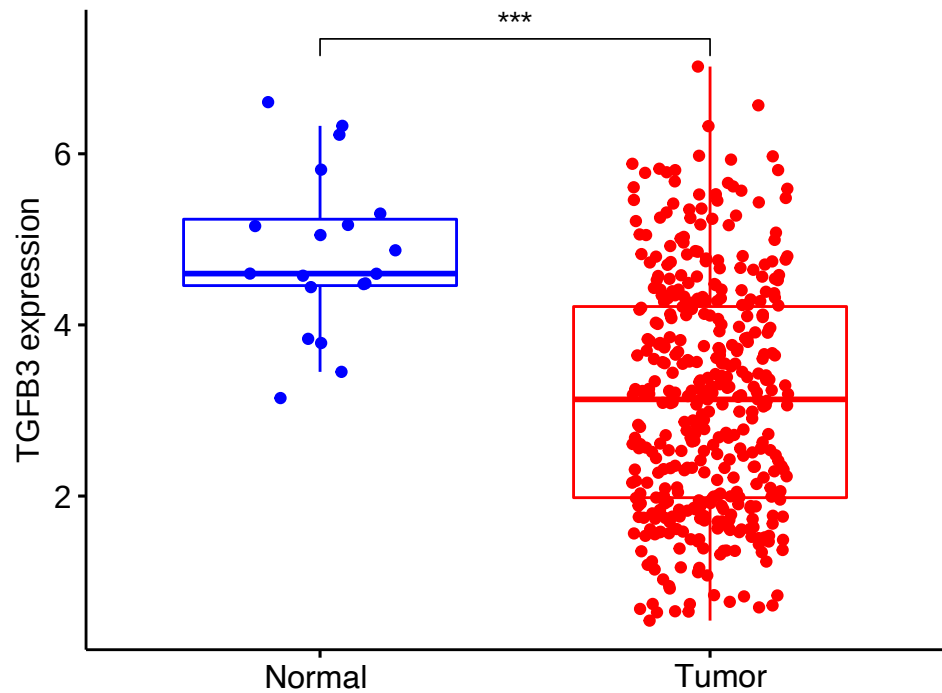


SPARCL1 expression

Normal Tumor



Normal Tumor

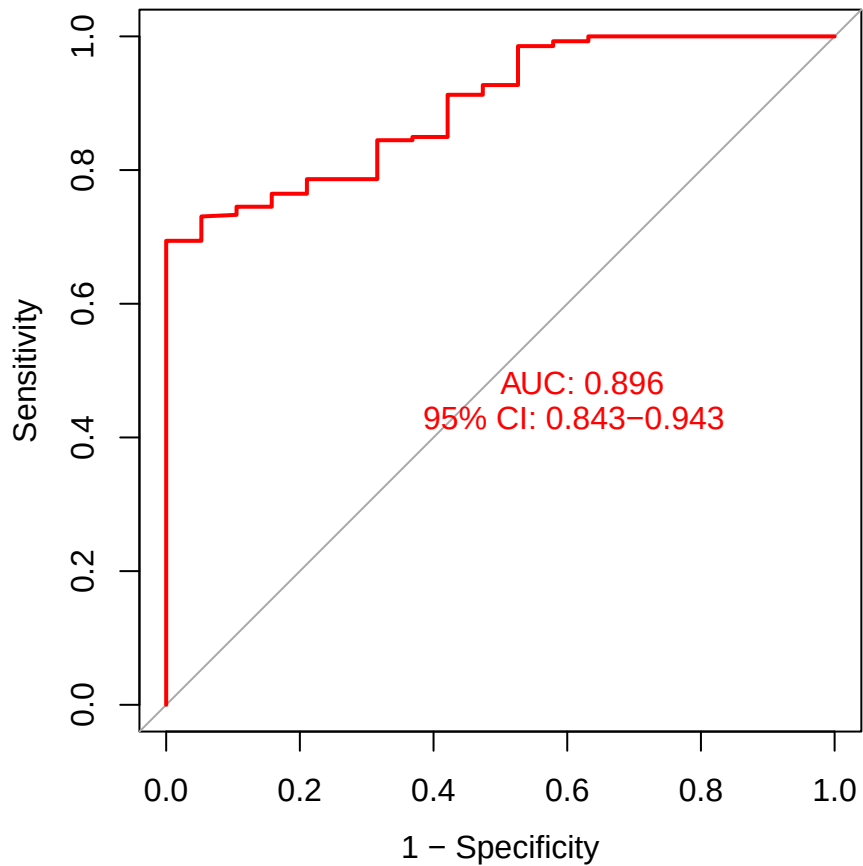


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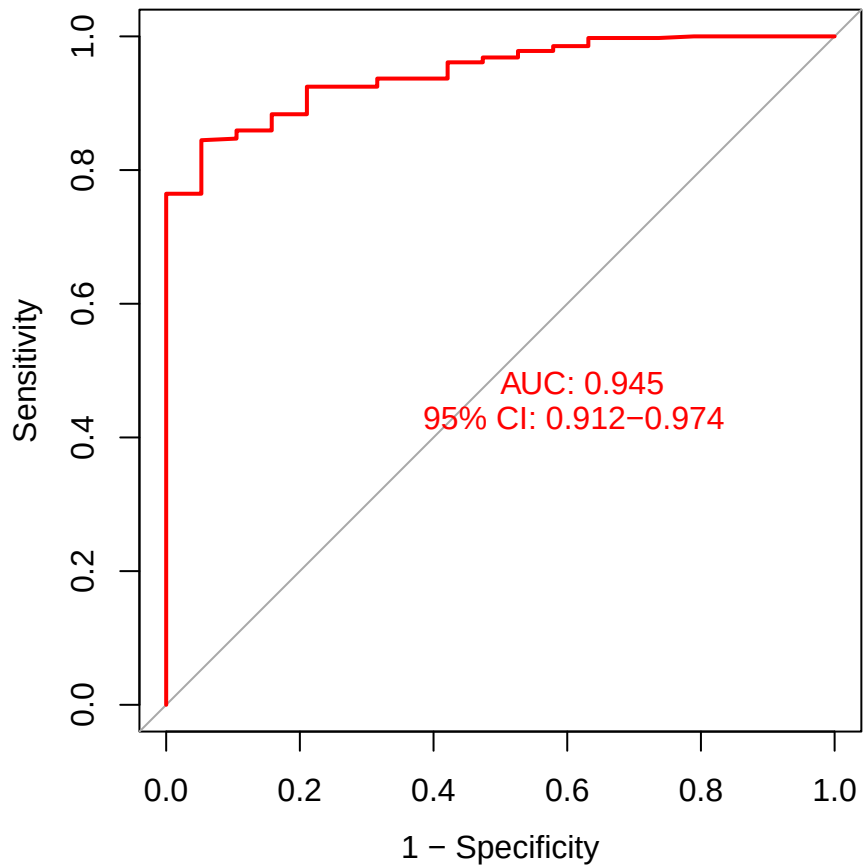
SUPPLEMENTARY MATERIAL 4

ROC curves of 14 genes as the diagnostic genes for BC in the
TCGA cohort

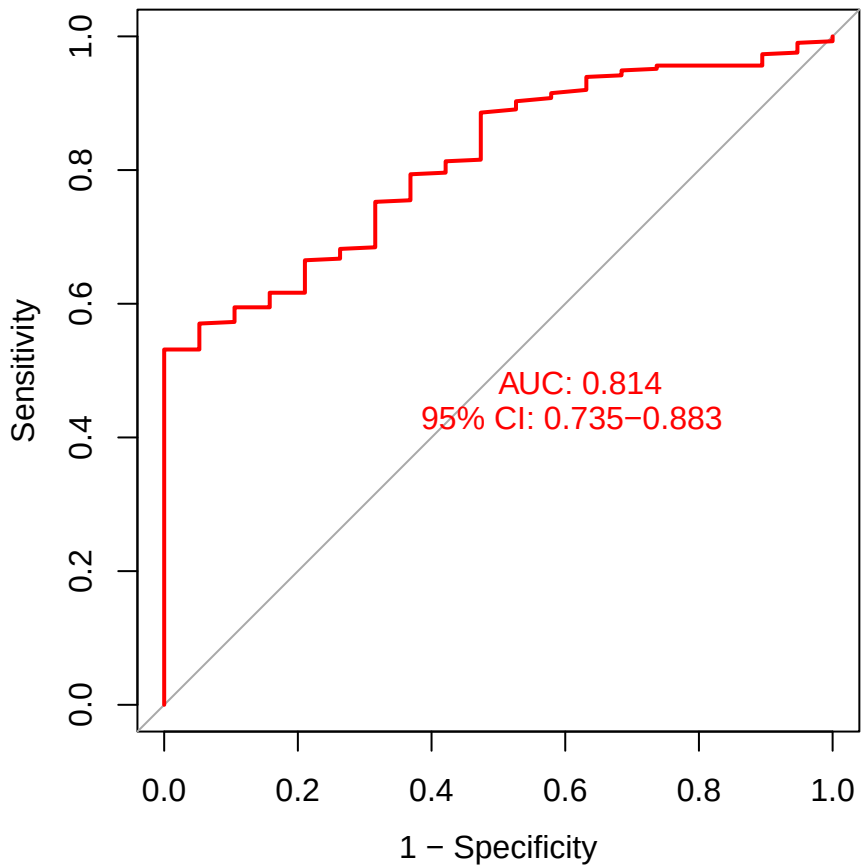
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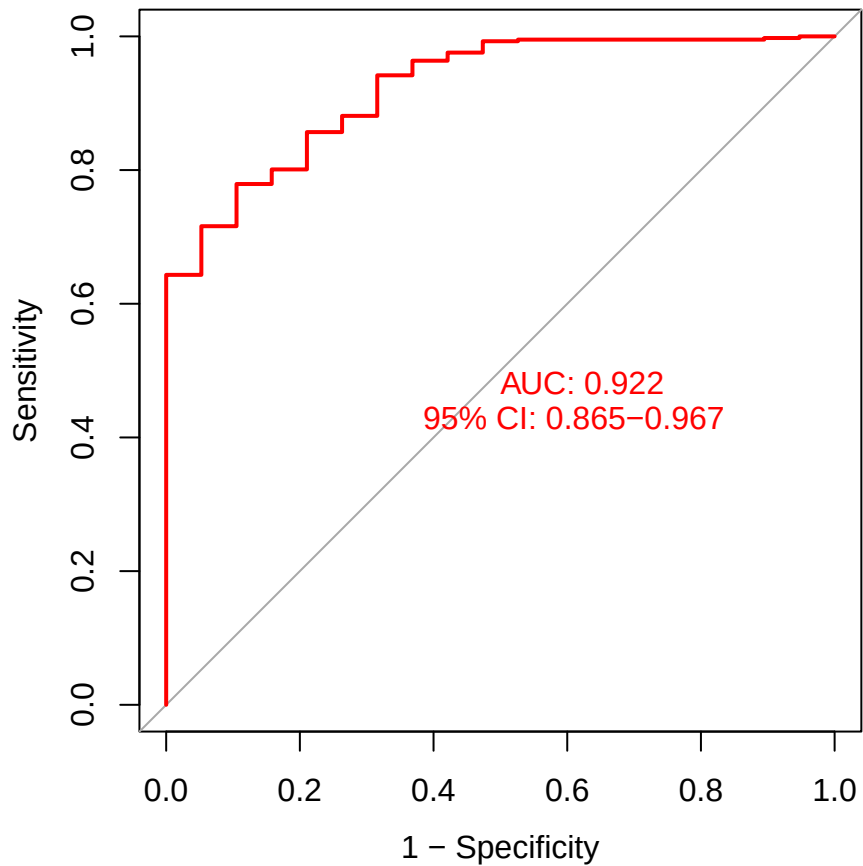
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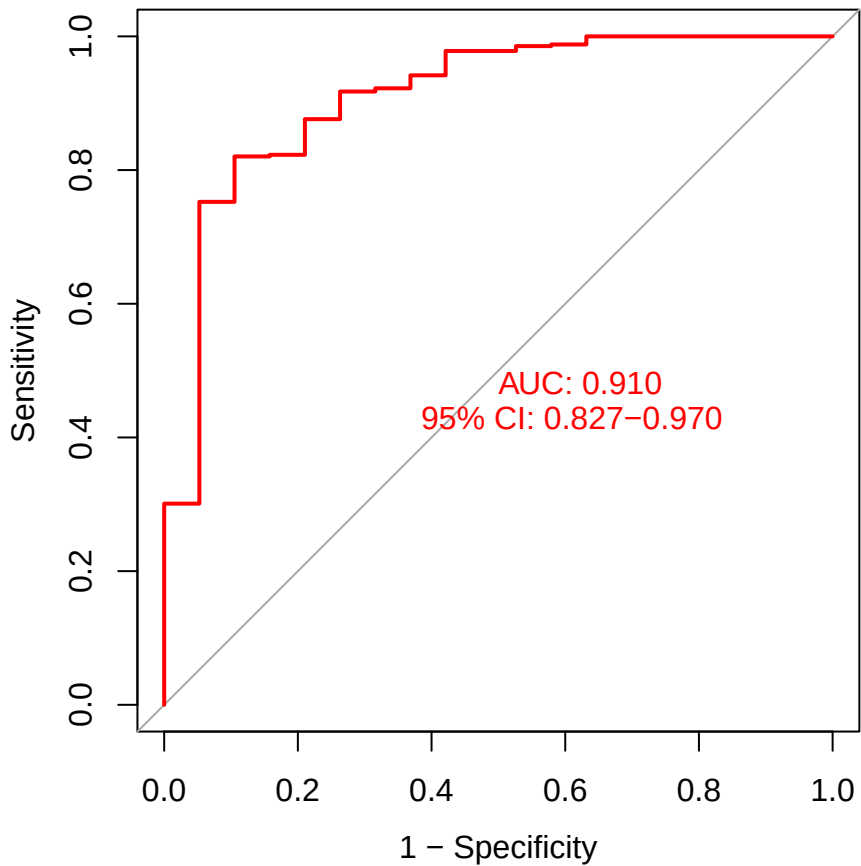
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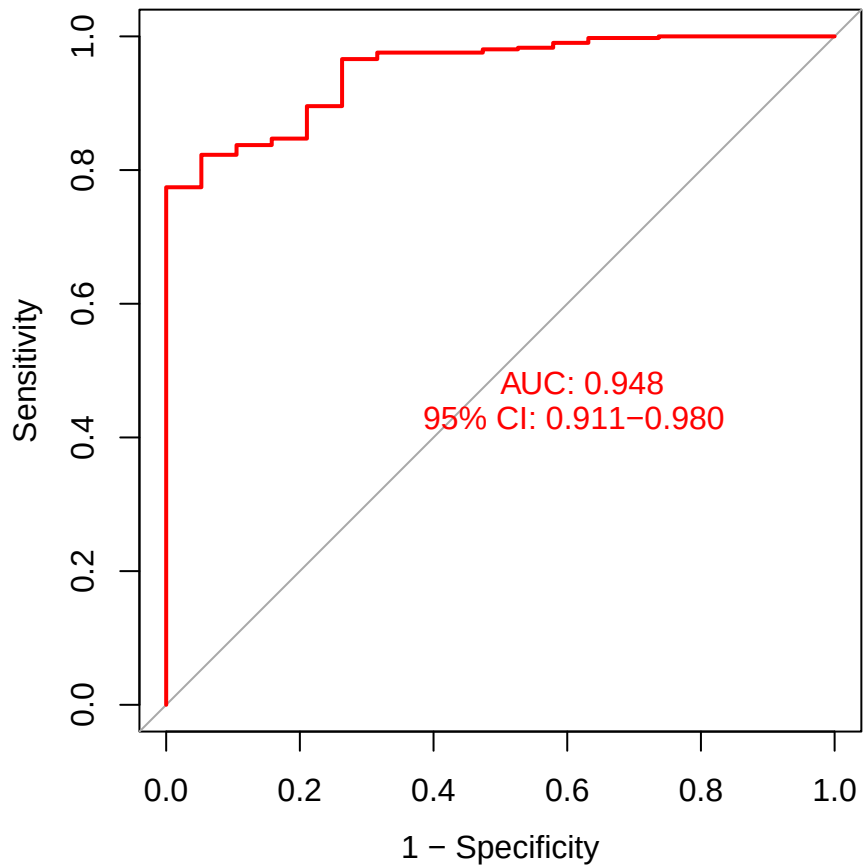
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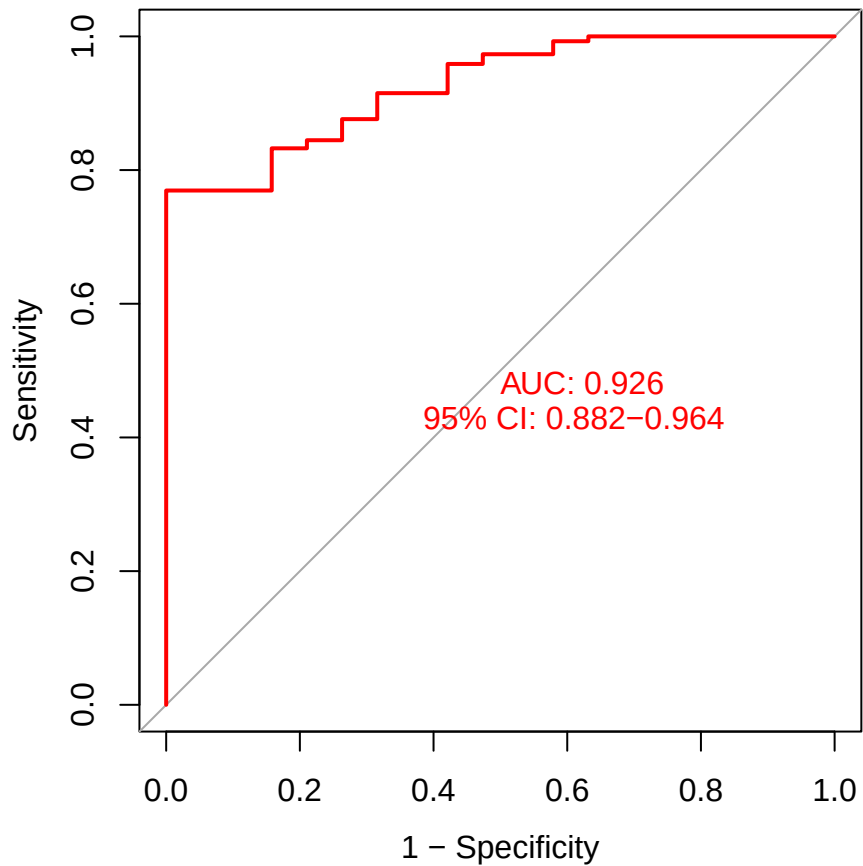
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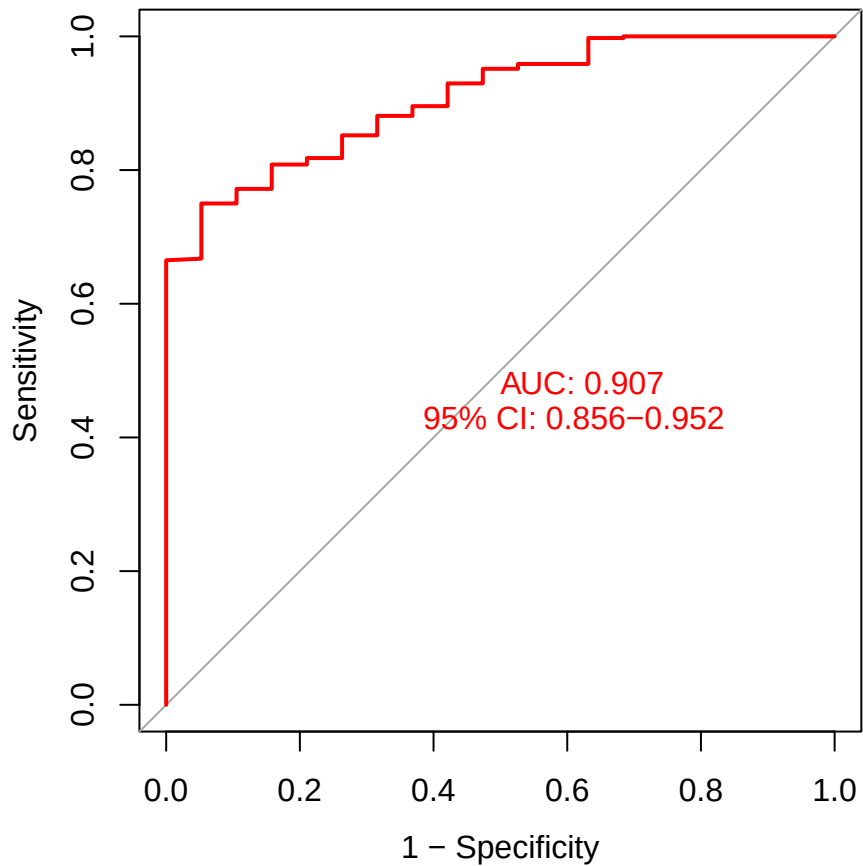
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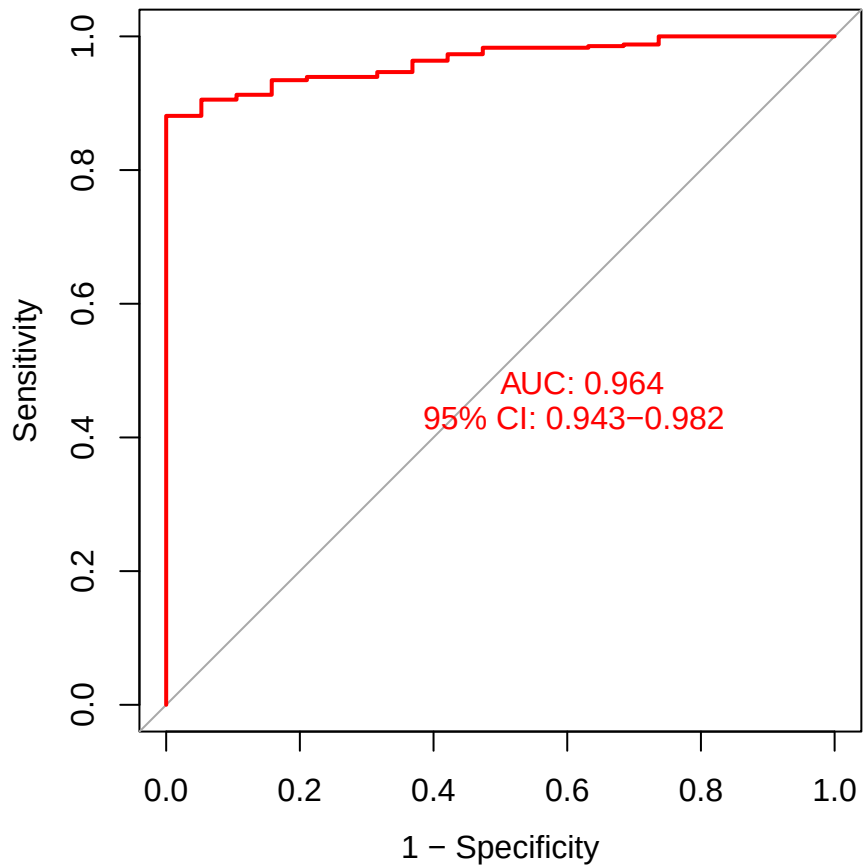
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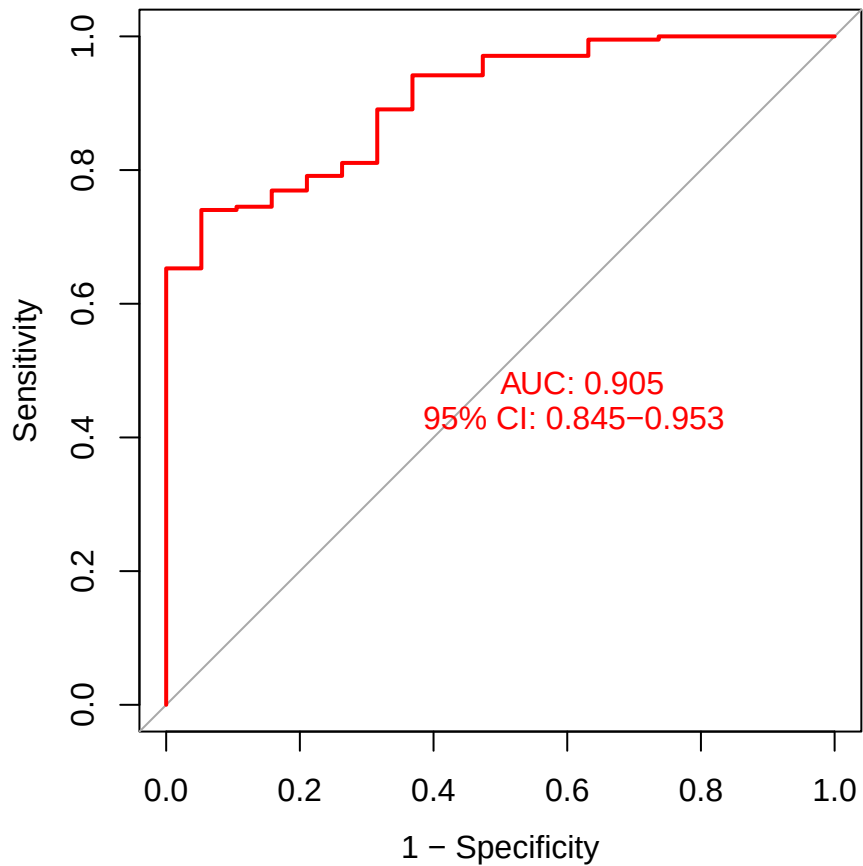
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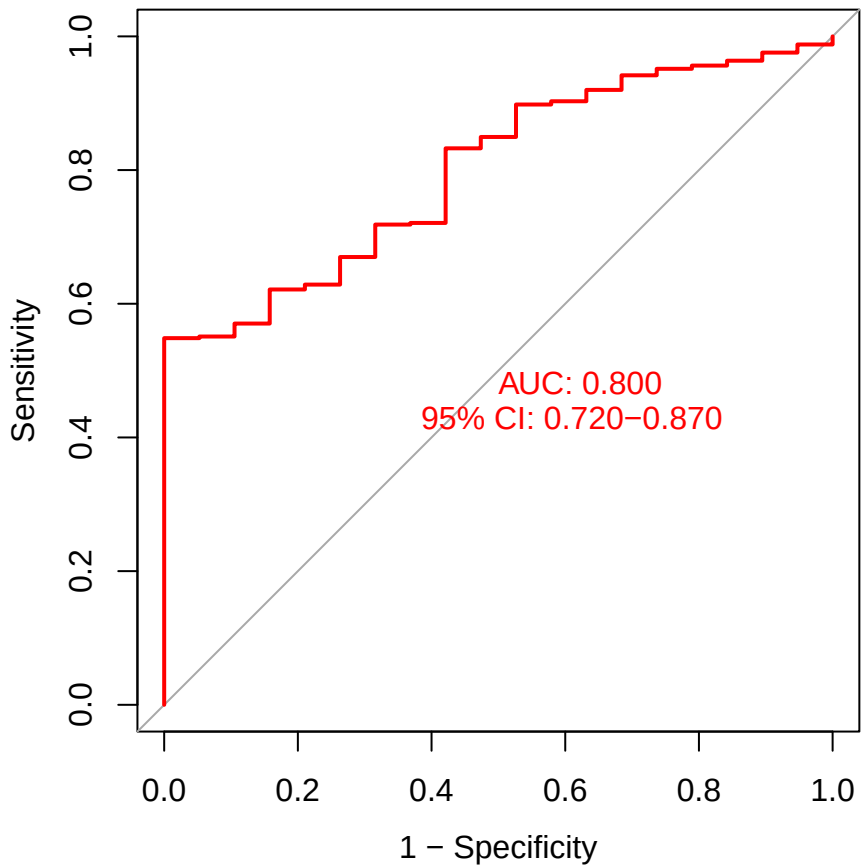
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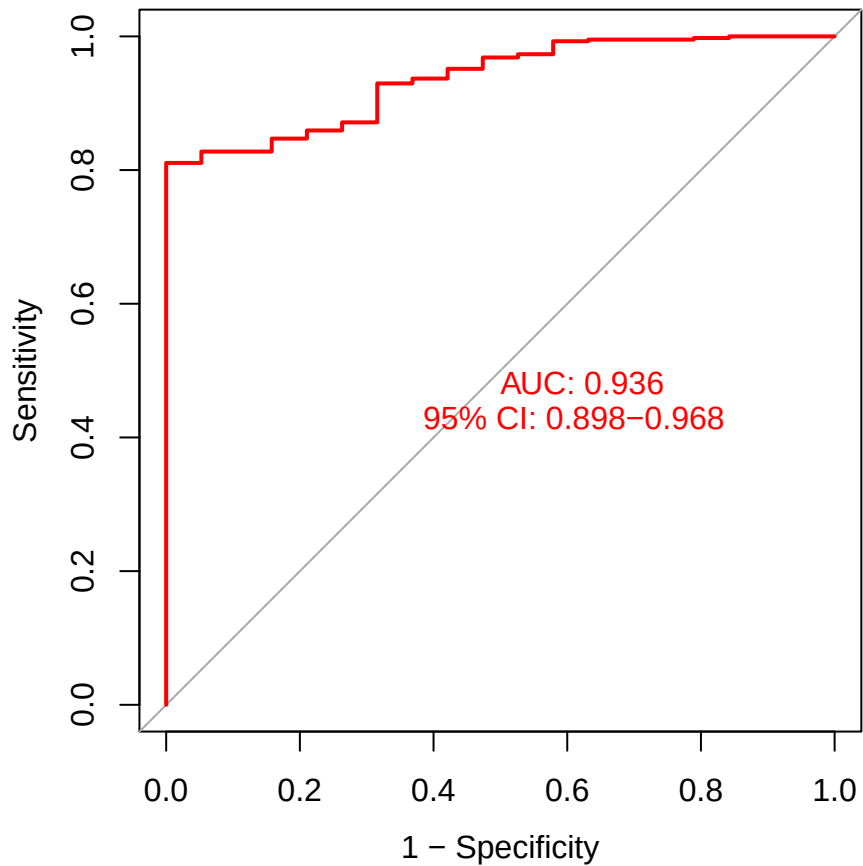
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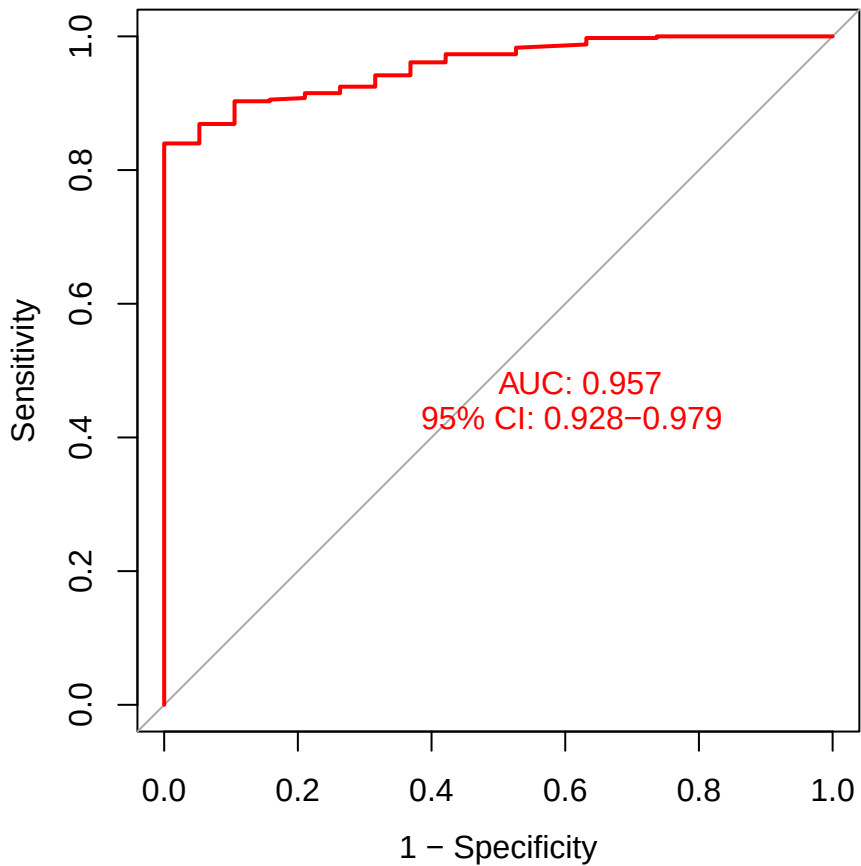
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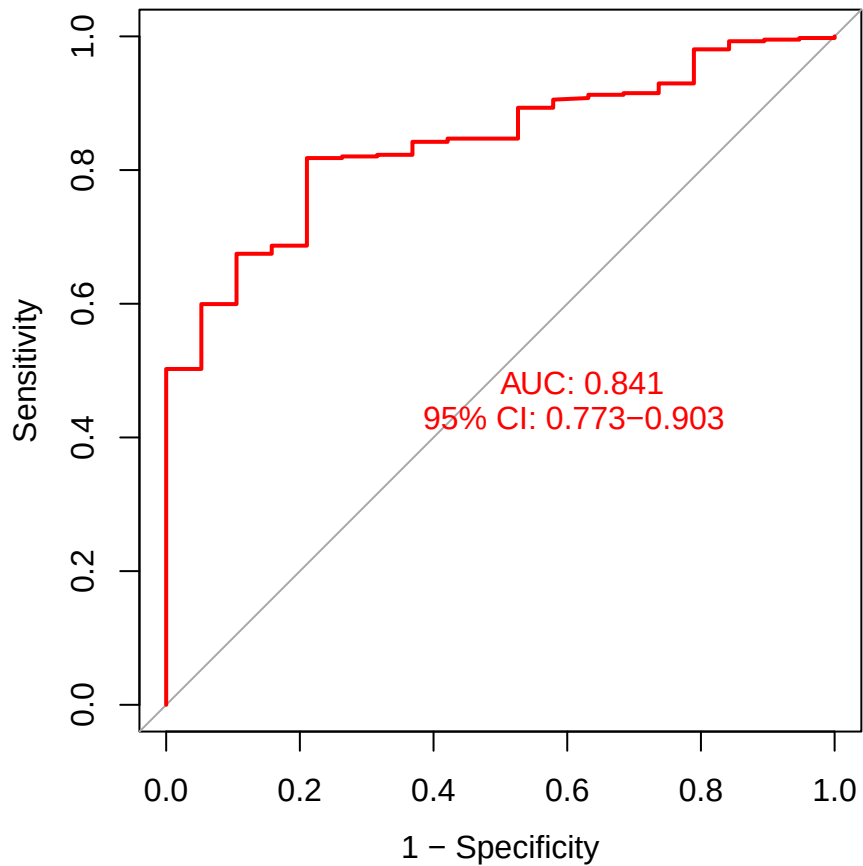
RASL12



SPARCL1



TGFB3



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SUPPLEMENTARY MATERIAL 5

275 genes which strongly correlated with JAM3

